

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 16:35:40 ; Search time 20 Seconds

(without alignments)  
1037.765 Million cell updates/sec

Title: US-09-454-651b-23

Sequence: 1 GLSHCSGVHYTKKEVKA.....LRVNTQFMNNTTKQEHFPDN 216

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 28338 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_71.\*  
2: PIR.\*  
3: PIR.\*  
4: PIR.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114.9	100.0	288	2 A45803	B-cell-restricted
2	108.5	94.4	289	2 G00031	B7 protein - red-c
3	73.8	64.2	239	2 I46690	CD80 precursor - r
4	601.5	52.3	321	2 I54766	B-lymphocyte activ
5	561	48.8	309	2 I49503	B-lymphocyte activ
6	185	16.1	275	2 JC7604	CD86 spliced varia
7	182	15.8	329	1 A48754	B7-2 antigen - hum
8	152	13.2	309	2 I49522	gene B7-2 protein
9	140.5	12.2	330	2 I46691	CD86 precursor - r
10	133.5	11.6	583	2 I39428	alcam - human
11	129	11.2	221	1 G0848	BARF1 protein - hu
12	127	11.1	526	2 S70587	butyrophilin precu
13	122.5	10.7	388	2 JH0506	adhesion molecule
14	122.5	10.7	588	2 A45254	surface glycoprote
15	120.5	10.5	509	2 JC5288	SHP substrate-1 pr
16	120.5	10.5	513	2 JC5289	SHP substrate-1 pr
17	118	10.3	487	2 S65133	butyrophilin - mou
18	116.5	10.1	1088	1 IUXLMU	neural cell adhesi
19	115	10.0	761	1 IJHUNG	neural cell adhesi
20	112.5	9.8	725	2 JE0059	neural cell adhesi
21	110.5	9.6	587	2 JH0464	DM-GRASP precursor
22	109.5	9.5	646	2 I38049	cell surface glyco
23	109.5	9.5	853	1 IJBONC	neural cell adhesi
24	109	9.5	526	2 A37821	butyrophilin - bov
25	109	9.5	2029	1 TDFELK	protein-tyrosine-p
26	108	9.4	871	1 I48696	protein-tyrosine k
27	107.5	9.4	5175	2 T20992	hypothetical prote
28	107.5	9.4	5198	2 T43290	hemiscentin precurs

30	106.5	9.3	333	2 A31923	amalgam protein pr
31	106.5	9.3	858	1 IJRTNG	neural cell adhesi
32	106	9.2	267	2 PL0064	T-cell receptor be
33	105.5	9.2	1091	1 IJCHNL	neural cell adhesi
34	104.5	9.1	210	2 A56169	Ig kappa chain V r
35	104	9.1	307	1 RWSBRC	T-cell receptor be
36	104	9.1	725	2 JE0100	neural cell adhesi
37	104	9.1	1092	1 JN0635	neural cell adhesi
38	103.5	9.0	480	2 A56182	fibroblast growth
39	103.5	9.0	725	1 IJMSNG	neural cell adhesi
40	103.5	9.0	1115	1 IJMSNL	neural cell adhesi
41	103	9.0	423	2 T29549	hypothetical prote
42	103	9.0	1273	2 T42405	sax-3 protein - Ca
43	102.5	8.9	503	2 JC5287	SHP substrate-1 pr
44	102	8.9	1443	2 I50600	neogenin - chicken
45	101	8.8	1033	2 S19247	cell adhesion prot

#### ALIGNMENTS

##### RESULT 1

A45803  
B-cell-restricted antigen B7 precursor - human  
N:Alternate names: B-lymphocyte activation antigen B7  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text, change 29-Sep-1999  
C:Accession: I54495; A45803  
R:Selvakumar, A.; Mohanraj, B.R.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.  
Immunogenetics 36, 175-181, 1992  
A:Title: Genomic organization and chromosomal location of the human gene encoding the  
A:Reference number: I54495; MUID:92307753  
A:Accession: I54495  
A:Status: translated from GB/EMBL/DBAJ  
A:Molecule type: DNA  
A:Residues: 1-288 <RES>  
A:Cross-references: GB:M83077; NID:q179327; PIDN:AAA58390.1; PID:q179329  
R:Freeman, G.J.; Freedman, A.S.; Segall, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.  
J. Immunol. 143, 2714-2722, 1989  
A:Title: B7, a new member of the Ig superfamily with unique expression on activated a  
A:Reference number: A45803; MUID:90010147  
A:Accession: A45803  
A:Molecule type: mRNA  
A:Residues: 1-288 <PRE>  
A:Cross-references: GB:M27533; NID:q184680; PIDN:AAA36045.1; PID:q306916  
C:Genetics:  
A:Gene: GDB:CD80; CD28LGL; CD28  
A:Cross-references: GDB:251792; OMIM:112203  
A:Map position: 3q13.3-3q21  
A:Introns: 34/1; 140/1; 234/1; 266/1  
C:Superfamily: B-lymphocyte restricted antigen B7  
C:Keywords: transmembrane protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 114.9; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 2.1e-85;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLSHCSGVHYTKKEVKAATLSCGHNVSEELAQTRTYWQEKRMVLTMMSGDNIMPE 60  
|||||  
DB 27 GLSHCSGVHYTKKEVKAATLSCGHNVSEELAQTRTYWQEKRMVLTMMSGDNIMPE 86  
OY 61 YKNRTIFDITNNLSIVIALRPSDEGTIECVYLKTEKDAFKREHLAEVTLISKADFPPTS 120  
|||||  
DB 87 YKNRTIFDITNNLSIVIALRPSDEGTIECVYLKTEKDAFKREHLAEVTLISKADFPPTS 146  
OY 121 ISDFELPTSNIRKICSTSGGPEPHLSLWLENGEELNATNTVSODPETELTAVSSKIDF 180  
|||||  
DB 147 ISDFELPTSNIRKICSTSGGPEPHLSLWLENGEELNATNTVSODPETELTAVSSKIDF 206  
OY 181 NMTTNHSEFACLIKYGHLRVNQTFFNMNTTKQEHFPDN 216  
|||||

Db 207 NMTHNSFMCLIKYGHRLRVNOTFMNTTCKOEHPPDN 242

# RESULT 2

G00031

B7 protein - red-crowned mangabey (fragment)  
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)  
C:Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 29-Sep-1999  
C:Accession: G00031

R.Villinger, F.J.

submitted to the EMBL Data Library, January 1995

A:Reference number: G00217

A:Accession: G00031

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-289 <YIL>

A:Cross-references: EMBL:019833; NID:g644783; PIDN:AAA86700.1; PID:g644784

A:Genetics:

A:Gene: B7

C:Superfamily: B-lymphocyte restricted antigen B7

## Query Match

Best Local Similarity 94.4%; Score 1085; DB 2; Length 289;  
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 2 LSHFSGVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEY 61

28 LSHFSGVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEY 87

Qy 62 KNTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 121

Db 88 KNTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 147

Qy 122 SPTETTSNIRRICSTSGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFN 181

Db 148 TPEELPPSNIRRICSTSGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFN 207

Qy 182 MTTNHSFMCILIKYGHRLRVNOTFMNTTCKOEHPPDN 216

Db 208 MTTNHSFMCILIKYGHRLRVNOTFMNTTCKOEHPPDN 242

RESULT 3

CD80 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 29-Sep-1999

C:Accession: I46690

R:Isson, T.; Seto, A.

Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule

A:Reference number: I46689; MUID:95369849

A:Accession: I46690

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-299 <ISO>

A:Cross-references: GB:049843; NID:g755096; PIDN:BA006643.1; PID:g755097

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match

Best Local Similarity 64.2%; Score 738; DB 2; Length 299;  
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

Db 4 HFGSVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEYKN 63

29 HFGSVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEYKN 88

Qy 64 RTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 123

Db 89 RTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 148

Qy 124 FEIPTNIRRICSTSGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFPNT 183

Db 149 IGHPDPNVKRIKRCASGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFPNT 208

Qy 184 TNHSEFMCLIKYGHRLRVNOTFMNTTCKOEHPPDN 211

Db 209 NMTHNSFMCLIKYGHRLRVNOTFMNTTCKOEHPPDN 242

RESULT 4

B-lymphocyte activation antigen 7-1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 19-May-2000

C:Accession: I54766

R:Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.

Int. Immunol. 7, 171-178, 1995

A:Title: Cloning the rat homolog of the CD28/CTLA-4 ligand B7-1: structural and funct

A:Reference number: I54766; MUID:95252184

A:Accession: I54766

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-321 <RES>

A:Cross-references: EMBL:005933; NID:g453381; PIDN:AAA80154.1; PID:g453382

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match

Best Local Similarity 52.3%; Score 601.5; DB 2; Length 321;  
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

Db 1 GLSHFSGVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEY 59

31 GLSHFSGVHTVREKEVATLSCGHNVSEELAOIRYQKKEKKVLTMMSGDMNIPPEY 90

Qy 60 EYKNTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 119

Db 91 EYKNTTIDITNNLSIVIALRPSDEGTVECVLTKYKDAFKREHLAEVLTSLVKADFPPTSI 150

Qy 120 SPTETTSNIRRICSTSGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFN 179

Db 151 SPTETTSNIRRICSTSGGFPPEPHLSWLENGELNAINTVSODPETELIYAVSSKIDFN 210

Qy 180 MTTNHSFMCILIKYGHRLRVNOTFMNTTCKOEHPPDN 205

Db 211 MTTNHSFMCILIKYGHRLRVNOTFMNTTCKOEHPPDN 242

RESULT 5

B-lymphocyte activation antigen 7 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 29-Sep-1999

C:Accession: I49503; S17291; I49521

R:Selyakumar, A.; White, P.C.; Dupont, B.

Immunogenetics 38, 292-295, 1993

A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.

A:Reference number: I49503; MUID:93307789

A:Accession: I49503

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-309 <RES>

A:Cross-references: GB:I42589; NID:g293299; PIDN:AAA37240.1; PID:g293301

R:Freeman, G.J.; Gray, G.S.; Glimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fling

J. Exp. Med. 174, 625-633, 1991

A:Title: Structure, expression, and T cell costimulatory activity of the murine homol

A:Reference number: S17291; MUID:913341422

A:Accession: S17291

A:Molecule type: mRNA

A:Residues: 1-274, R, 279-309 <RES>

A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112

R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.

Biochem. Biophys. Res. Commun. 200, 443-449, 1994

A:Title: Identification of an alternatively spliced form of the murine homologue of B

A:Reference number: I49521; MUID:94220123

A:Accession: I49521  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-143,238-274,'R',279-309 <RE2>  
A:Cross-references: GB:D16220; NID:g505118; PIDN:BA03748.1; PID:g994769  
C:Genetics:  
A:Gene: B7  
A:Introns: 37/1; 143/1; 237/1; 275/1  
C:Superfamily: B-lymphocyte restricted antigen B7  
C:Keywords: alternative splicing

Query Match 48.8%; Score 561; DB 2; Length 309;  
Best Local Similarity 50.7%; Pred. No. 6,6e-38;  
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTEKEVATLSCGHNVSYVELAOTRIYMOKEKKMYLTMM---SGDMNIMPEYKNTIFDI 71  
DB 42 LSSVYDKVLLPCRYNPHDESDRIYMOKHDKVYLSVLAGKLVPEYKNTIYDNT- 100  
QY 72 NLSIVILALRPDSGEYECVLYEKDAFRHLAEVTLVSKADFPPTPSISDFEIPTSNI 131  
DB 101 TYSILILGLVLSRGYSCVYOKKERGTVEKHLALVKLSIKADFPPTNITESGNPSADT 160  
QY 132 RRIICSTSGGFPPEHLSWLNGEELNINTVSQDPETELAVSSKIDFNMTTHSFMCL 191  
DB 161 KRITCFASGGFPKPRSWLNELGRELPIINTTISODPESELTYSQDPETNTHNTKCL 220  
QY 192 IKYGLHVNQTFNNMTTKOEHFDPN 216  
DB 221 IKYGDHVSDFMTWEKPEDEP-PDS 244

## RESULT 6

JC7604  
CD86 spliced variant CD86 delatam isoform - human

C:Species: Homo sapiens (man)  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001  
C:Accession: JC7604  
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.  
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001  
A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.  
A:Reference number: JC7604; MUID:21092744; PMID:11162656  
A:Accession: JC7604  
A:Molecule type: mRNA  
A:Residues: 1-275 <MAG>  
C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory  
C:Genetics:  
A:Gene: cd86delatam  
C:Keywords: immune response

Query Match 16.1%; Score 185; DB 2; Length 275;  
Best Local Similarity 27.4%; Pred. No. 1.3e-07;  
Matches 65; Conservative 42; Mismatches 78; Indels 52; Gaps 12;

QY 18 EVATLSC---GHNVSYVELAOTRIYMOKEKKMYLTMM---SGDMNIMPEYKNTIFDI 69  
DB 28 ETALPPOFANSQOSSELY---VEMQDQENLVLENYLKEKFDVSHSKYMGRTSFD- 83  
QY 70 TNNLSIVILALRPDSGEYECVLYEKDAFRHLAEVTLVSKADFPPTPSISDFEIPTS 129  
DB 84 SDSMTLRLHNLQIDKGLYCCIIHKKRPTGMIRIHONNSELVLANFSQPEI---VPIS 139  
QY 130 NIR-----RIICSTSGGFPPEHLSWLNGEELNINTV-----SODPEELAVS 175  
DB 140 NITENVYINLCCSIHGPPEPKMSVL-----LRTKNSITIEDGIMOKSQDNVTELDVS 194  
QY 176 SKLDF---NMTNHSFMCILIKYGLHVNQ---TFNWNNTTKOE-----FPD 215  
DB 195 ISLSVSPDVTSMNTIFCIETDKTRLSPFSIGTINMESEBQTKRKRIHPE 251

RESULT 7  
A48754

B7-2 antigen - human  
N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48754; S39055  
R:Freeman, G.J.; Gribben, J.G.; Boussois, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard  
Science 262, 909-911, 1993  
A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr  
A:Reference number: A48754; MUID:94053735  
A:Accession: A48754  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-329 <RES>  
A:Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369  
A:Note: It is uncertain whether Met-1 or Met-7 is the initiator  
R:Aizumi, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,  
Nature 366, 76-79, 1993  
A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.

A:Reference number: S39055; MUID:94050123  
A:Accession: S39055  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 7-329 <AZU>  
A:Cross-references: GB:U04343; NID:g439838; PIDN:AA03814.1; PID:g439839  
C:Genetics:  
A:Gene: GDB:CD86; CD28LG2  
A:Cross-references: GDB:433597; OMIM:601020  
A:Map position: 3q13.3-q21  
C:Superfamily: B7-2 antigen  
C:Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;  
Best Local Similarity 29.0%; Pred. No. 2.7e-07;  
Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;

QY 18 EVATLSC---GHNVSYVELAOTRIYMOKEKKMYLTMM---SGDMNIMPEYKNTIFDI 69  
DB 34 ETALPPOFANSQOSSELY---VEMQDQENLVLENYLKEKFDVSHSKYMGRTSFD- 89  
QY 70 TNNLSIVILALRPDSGEYECVLYEKDAFRHLAEVTLVSKADFPPTPSISDFEIPTS 129  
DB 90 SDSMTLRLHNLQIDKGLYCCIIHKKRPTGMIRIHONNSELVLANFSQPEI---VPIS 145  
QY 130 NIR-----RIICSTSGGFPPEHLSWLNGEELNINTV-----SODPEELAVS 175  
DB 146 NITENVYINLCCSIHGPPEPKMSVL-----LRTKNSITIEDGIMOKSQDNVTELDVS 200  
QY 176 SKLDF---NMTNHSFMCILIKYGLHVN 199  
DB 201 ISLSVSPDVTSMNTIFCIETDKTRL 227

## RESULT 8

gene B7-2 protein - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I49522  
R:Freeman, G.J.; Borteljo, F.; Hodges, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim  
J. Exp. Med. 178, 2185-2192, 1993  
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell  
A:Reference number: I49522; MUID:94065585  
A:Accession: I49522  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-309 <RES>  
A:Cross-references: GB:L25606; NID:g432478; PIDN:AA079770.1; PID:g432479  
C:Genetics:  
A:Gene: B7-2  
C:Superfamily: B7-2 antigen

Query Match 13.2%; Score 152; DB 2; Length 309;  
Best Local Similarity 26.1%; Pred. No. 6.7e-05;



Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKREALTSC--GINVSYEEALAQRIITWQKKKMYLTMGSG---DMNIPYKKNITF--- 67  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 42 VGDAELPCRLSPNASEHL-ELRWFRRKSPYLVHRDREGAEQMPERGRATLVOD 100  
 QY 68 -DITNNLSIYLALRPSDEGTGYCVLKYKDAFKREHLAEVTLVSKADPTPTSPISFEI 126  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 101 GIKGRVALRIRGVRSDDOETCF--FREDSSYEAL--VHLKVALGSDPHIS-MQV 154  
 QY 127 PISNIRITITSGGPEPHLSM-LENGEELNAINTVSODPETE-LYAVSSKIDFNMPT 184  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 155 QENGEICLECTSGVWPEPQVQWRTSNGEKF--STSESNNPDEGLFTVAASYIINDTS 212  
 QY 185 NHSFMCILK 193  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 213 TRNVSCYIQ 221

## RESULT 13

JH0506

adhesion molecule SC1 precursor - chicken

C:Species: Gallus gallus (chicken)

C&gt;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jul-2000

C:Accession: JH0506; PS0270

R:Ranka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.;

Neuron 7, 535-545, 1991

A:Title: Molecular cloning and expression of a novel adhesion molecule, SC1.

A:Reference number: JH0506; M0ID:92030150

A:Accession: JH0506

A:Residues: 1-588 &lt;TRAN&gt;

A:Cross-references: GB:S63276; NID:9238000; PIDN:AAB20170.1; PID:9238001

A:Experimental source: embryo

A:Accession: PS0270

A:Molecule type: protein

A:Residues: 34-48 &lt;TRAN&gt;

C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons

C:Keywords: glycoprotein; transmembrane protein

F:1-33/Domain: signal sequence #status predicted &lt;SIG&gt;

F:34-388/Product: adhesion molecule SC1 #status predicted &lt;ADH&gt;

F:500-523/Domain: transmembrane #status predicted &lt;TRA&gt;

F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match

Best Local Similarity 10.7%; Score 122.5; DB 2; Length 588;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEYKNTIFDITNNLSIVILALRPSDEGTGYCVLKYKDAFKREHLAEVTLVSKADPT 118  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 90 PDVKDR--LSLSNVTYLSIKMARISDEKRFVCM-LVT-EDVSEEPYVKK-----FKQ 139  
 QY 119 PS-----ISDFEIPISNIRI-ICSTSGGPEPHLSWLENG-----EELNAINTVSQ 165  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 140 PSQPEILHQADF-LETEKLMKLGECVVRDSEYPCGNVTWYKNGRVLQVEEVVYINLKEVE 198  
 QY 166 DPETELXAVSSKIDFNMPT--TNHSMCLIKY 194  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 199 NRSTGLFTMTSSLOQYMPTEKEDANAKFTCIATY 230

## RESULT 14

A45254

surface glycoprotein BEN precursor - chicken

C:Species: Gallus gallus (chicken)

C&gt;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jul-2000

C:Accession: A45254; S19202

R:Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992

A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in

A:Reference number: A45254; M0ID:92302224

A:Accession: A45254

A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Query Match

Best Local Similarity 10.7%; Score 122.5; DB 2; Length 588;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEYKNTIFDITNNLSIVILALRPSDEGTGYCVLKYKDAFKREHLAEVTLVSKADPT 118  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 90 PDVKDR--LSLSNVTYLSIKMARISDEKRFVCM-LVT-EDVSEEPYVKK-----FKQ 139  
 QY 119 PS-----ISDFEIPISNIRI-ICSTSGGPEPHLSWLENG-----EELNAINTVSQ 165  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 140 PSQPEILHQADF-LETEKLMKLGECVVRDSEYPCGNVTWYKNGRVLQVEEVVYINLKEVE 198  
 QY 166 DPETELXAVSSKIDFNMPT--TNHSMCLIKY 194  
 A:Residues: 1-588 <TRAN>  
 A:Cross-references: EMBL:X64301; NID:963087; PIDN:CAA45579.1; PID:963088  
 C:Keywords: glycoprotein

Db 199 NRSTGLFTMTSSLOQYMPTEKEDANAKFTCIATY 230

## RESULT 15

JC5288

SHP substrate-1 protein, 509 - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000

C:Accession: JC5288

R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioaka,

Biochem. Biophys. Res. Commun. 231, 61-67, 1997

A:Title: Mouse and human SHP-1: Molecular cloning of cDNAs and chromosomal localization

A:Reference number: JC5287; M0ID:97223399

A:Accession: JC5288

A:Residues: 1-509 &lt;YAM&gt;

A:Molecule type: mRNA

A:Cross-references: DDBJ:87967; NID:91864012; PIDN:BA13520.1; PID:91864013

C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

acts as a docking protein and induce translocation of SHP-2 from the cytosol to the

C:Genetics:

A:Gene: shps-1

A:Map position: 2

Query Match

Best Local Similarity 10.5%; Score 120.5; DB 2; Length 509;

Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

QY 3 SHFCSGV----IHVTKRVEVA-----TLSCGHNVSEELAQRIITWQKK--EKKMVL 48  
 A:Residues: 1-509 <YAM>  
 A:Cross-references: DDBJ:87967; NID:91864012; PIDN:BA13520.1; PID:91864013  
 C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

Db 23 SCFTGYTGKELKVTQPEKSYSAAGSTVINC---TLTSLIPVGPITKWRGVQSKILI 79  
 QY 49 TMSGDMNIMPEYKKNRTIFDIT--NML--SIVILALRPSDEGTGYCVLKYKDAFKREH 104  
 A:Residues: 1-509 <YAM>  
 A:Cross-references: DDBJ:87967; NID:91864012; PIDN:BA13520.1; PID:91864013  
 C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

Db 80 YSFGEH--PPRYTN--VSDATKNNMDFSLRSINVPEDAGTYCV--KQKQPSPTD 133  
 QY 105 L-----AEVTLVSKADFPSPS--ISDFEIPISNIRI-ICSTSGGPEPHLSWLENGEEL 156  
 A:Residues: 1-509 <YAM>  
 A:Cross-references: DDBJ:87967; NID:91864012; PIDN:BA13520.1; PID:91864013  
 C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

Db 134 EIOGGGTEVYVLAKPSPPEVSGPADRGIPDQK-NEFCCKSHGSPSPNITLWKFKDQEL 192  
 QY 157 NAINTVSODPETELXAVSS--KIDFNMPTTNHSMCLIKYGLHVNQV 202  
 A:Residues: 1-509 <YAM>  
 A:Cross-references: DDBJ:87967; NID:91864012; PIDN:BA13520.1; PID:91864013  
 C:Comment: This protein is a glycosylated receptor-like protein and plays a role in c

Db 193 HHLETTYVPSGKNVSYNISSTVRYVLSMDVHS-KVCEVAHITLDS 239

Search completed: October 17, 2002, 16:37:21  
 Job time : 22 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 16:35:40 ; Search time 13 Seconds

(without alignments)  
643.340 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVHHTKEVKA.....LRFVNTFNMTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80_HUMAN
2	738	64.2	299	1	CD80_RABIT
3	561	48.8	306	1	CD80_MOUSE
4	182	15.8	329	1	CD86_HUMAN
5	161	14.0	302	1	ICD1_HUMAN
6	152	13.2	309	1	CD86_MOUSE
7	150.5	13.1	322	1	ICD1_MOUSE
8	140.5	12.2	330	1	CD86_RABIT
9	134.5	11.7	583	1	C166_MOUSE
10	133.5	11.6	583	1	C166_HUMAN
11	129	11.2	221	1	BRL1_EBV
12	127	11.1	526	1	BUTY_HUMAN
13	122.5	10.7	588	1	C166_CHICK
14	119	10.4	524	1	BUTY_MOUSE
15	116.5	10.1	1088	1	NCAL_XENLA
16	115	10.0	761	1	NCAL_HUMAN
17	115	10.0	848	1	NCAL_HUMAN
18	110.5	9.6	321	1	TCB_FAV
19	109.5	9.5	646	1	NCAL_HUMAN
20	109.5	9.5	853	1	NCAL_BOVIN
21	109	9.5	526	1	BUTY_BOVIN
22	109	9.5	2029	1	LAR_DROME
23	108.5	9.4	365	1	CXR_MOUSE
24	107.5	9.4	333	1	AMAL_DROME
25	106.5	9.3	858	1	NCAL_RAT
26	105	9.1	319	1	A33_HUMAN
27	105	9.1	1091	1	NCAL_CHICK
28	104	9.1	1092	1	NCAL_MOUSE
29	103.5	9.0	725	1	NCAL_MOUSE
30	103.5	9.0	1115	1	NCAL_MOUSE
31	103	8.9	298	1	JAM2_HUMAN
32	102	8.9	1443	1	NEO1_CHICK
33	101.5	8.8	403	1	RAGE_MOUSE

34	100	8.7	413	1	HEMO_MANSE
35	99.5	8.7	1338	1	VGR1_HUMAN
36	98.5	8.6	365	1	CXR_HUMAN
37	98	8.5	278	1	OX2G_RAT
38	98	8.5	298	1	JAM1_BOVIN
39	98	8.5	1333	1	VGR1_MOUSE
40	97	8.4	1336	1	VGR1_RAT
41	96.5	8.4	739	1	VCA1_HUMAN
42	96	8.4	1020	1	CONT_MOUSE
43	95.5	8.3	811	1	FS21_DROME
44	95.5	8.3	873	1	FS21_DROME
45	95.5	8.3	1348	1	VGR2_COTJA

## ALIGNMENTS

RESULT 1  
CD80\_HUMAN STANDARD; PRT; 288 AA.  
AC P33681;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BBI).  
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoid;  
RX MEDLINE=90010147; PubMed=2794510;  
RA Freeman G.J., Freedman A.S., Segal J.M., Lee G., Whitman J.F., Nadler L.M.;  
RT "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells."  
RT J. Immunol. 143:2714-2722(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92307753; PubMed=1377173;  
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;  
RT "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."  
RT Immunogenetics 36:175-181(1992).  
RN [3]  
RP SEQUENCE OF 35-38.  
RX MEDLINE=91341422; PubMed=1714935;  
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;  
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7."  
RT J. Exp. Med. 174:625-631(1991).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=95088403; PubMed=7527824;  
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;  
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."  
RT J. Immunol. 154:97-105(1995).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.  
RX MEDLINE=20125021; PubMed=10661405;  
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.Y., Stuart D.I., Davis S.J.;  
RT "Structure and dimerization of a soluble form of B7-1."  
RT Immunity 12:51-60(2000).  
CC 1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS  
CC RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES  
CC AND DENDRITIC CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M27533; AAA56045.1; -  
CC EMBL: M63077; AAA58390.1; -  
CC EMBL: M63072; AAA58390.1; JOINED.  
CC EMBL: M63073; AAA58390.1; JOINED.  
CC EMBL: M63074; AAA58390.1; JOINED.  
CC PIR: A45803; A45803.  
CC PDB: 1D89; 1D-JAN-01.  
CC MIM: 112203; -  
CC InterPro: IPR003599; Ig.  
CC InterPro: IPR003006; Ig\_MHC.  
CC InterPro: IPR003600; Ig\_Like.  
CC Pfam: PF00047; Ig; 1.  
CC SMART: SM00409; Ig; 1.  
CC SMART: SM00410; Ig\_Like; 1.  
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
CC Receptor; 3D-structure.  
CC SIGNAL 1 34  
CC FT CHAIN 35 288 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.  
CC FT DOMAIN 35 262 EXTRACELLULAR (POTENTIAL).  
CC FT TRANSMEM 243 263 POTENTIAL.  
CC FT DOMAIN 264 288 CYTOPLASMIC (POTENTIAL).  
CC FT DOMAIN 43 123 IG-LIKE V-TYPE DOMAIN.  
CC FT DOMAIN 155 223 IG-LIKE C2-TYPE DOMAIN.  
CC FT DISULFID 50 116  
CC FT DISULFID 162 216  
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 288 AA; 33048 MW; BAA53EE34528B1F4 CRC64;  
Query Match 100.0%; Score 1149; DB 1; Length 288;  
Best Local Similarity 100.0%; Pred. No. 3.5e-89;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
CD80\_RABIT  
ID CD80\_RABIT STANDARD; PRT: 299 AA.  
AC P42070;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1  
DE antigen).  
GN CD80.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_Taxid=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B/U X CHB;HM;  
RX MEDLINE=95369849; PubMed=7642234;  
RA Isono T., Seto A.;  
RT "Cloning and sequencing of the rabbit gene encoding T-cell  
RT costimulatory molecules";  
RL Immunogenetics 42:217-220(1995).  
CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T  
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE  
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS  
CC RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
CC  
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CC  
CC EMBL: D49843; BAA08643.1; -  
CC InterPro: IPR003599; Ig.  
CC InterPro: IPR003006; Ig\_MHC.  
CC InterPro: IPR003600; Ig\_Like.  
CC Pfam: PF00047; Ig; 1.  
CC SMART: SM00409; Ig; 1.  
CC SMART: SM00410; Ig\_Like; 1.  
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
CC Receptor.  
CC SIGNAL 1 32  
CC FT CHAIN 33 299  
CC FT DOMAIN 33 243 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.  
CC FT TRANSMEM 244 264 EXTRACELLULAR (POTENTIAL).  
CC FT DOMAIN 265 299 POTENTIAL.  
CC FT DOMAIN 42 122 CYTOPLASMIC (POTENTIAL).  
CC FT DOMAIN 154 222 IG-LIKE V-TYPE DOMAIN.  
CC FT DISULFID 49 115 IG-LIKE C2-TYPE DOMAIN.  
CC FT DISULFID 161 215 POTENTIAL.  
CC FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 299 AA; 33513 MW; 6744223E5C91DE0 CRC64;  
Query Match 64.2%; Score 738; DB 1; Length 299;  
Best Local Similarity 63.9%; Pred. No. 8.9e-55;  
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;



```

DB      29 HSSSGISQVTKSVKEMAAALSCDYNISIDELARMRIRYQKQDQAVLITISQVEMWEYKN 88
QY      64 RTFEDTNNIYIYIALRPDECTECVYLKYKDAFKREHLAEVTLVSADPEPSISD 123
DB      89 RTFPDINNLSLWILRLSDKTYCVQKNGNSFRFRHLVSVLISADPVPVSTID 148
QY      124 FELPTSNIRRIICSTSGGPEPHLSMLENGEELNAINTVSODETELAVAVSSKLDENMT 183
DB      149 IGHDPNVRKIRCSASGGPEPEPLAMNDEDELNAVTVTDQDLDFELYSVSELDENVIT 208
QY      184 TNHSEFCLIKYGLHRYNQTFNNMTTKOE 211
DB      209 NMHSIVCLIKYGLSVSOLFPMSPKROE 236

RESULT 3
CD80_MOUSE STANDARD; PRT; 306 AA.
ID      CD80_MOUSE
AC      000609;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE      antigen) (B7).
GN      CD80 OR B7.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-B-cell;
RX      MEDLINE=91341422; PubMed=1714935;
RA      Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA      White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT      "Structure, expression, and T cell costimulatory activity of the
RT      murine homologue of the human B lymphocyte activation antigen B7.";
RT      J. Exp. Med. 174:625-631(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE-B-cell;
RX      MEDLINE=93307789; PubMed=7686531;
RA      Selvakumar A., White P.C., Dupont B.;
RT      "Genomic organization of the mouse B-lymphocyte activation antigen
RT      B7.";
RT      Immunogenetics 38:292-295(1993).
CC      -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC      LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC      PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC      RECEPTOR.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC      INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC      MALIGNANCIES.
CC      -1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC      ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC      IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC
CC      EMBL: X60958; CAA43291.1; -
CC      DR      EMBL: L12589; AAA37240.1; ALT_SEQ.
CC      DR      EMBL: L12585; AAA37240.1; JOINED.

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DR      EMBL: L12586; AAA37240.1; JOINED.
DR      EMBL: L12587; AAA37240.1; JOINED.
DR      EMBL: L12588; AAA37240.1; JOINED.
DR      PIR: S17291; S17291.
DR      MGI: MGI:101775; Cd80.
DR      InterPro: IPR003599; Ig.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003600; Ig_Like.
DR      Pfam: PF00047; Ig_2.
DR      SMART: SM00409; Ig; 1.
DR      SMART: SM00410; Ig_Like; 1.
KW      Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW      Receptor.
FT      SIGNAL 1 37
FT      CHAIN 38 306
FT      DOMAIN 38 246
FT      TRANSMEM 247 268
FT      DOMAIN 269 306
FT      DOMAIN 47 126
FT      DOMAIN 158 226
FT      DOMAIN 227 246
FT      DISULFID 54 119
FT      DISULFID 165 219
FT      CARBOHYD 93 93
FT      CARBOHYD 99 99
FT      CARBOHYD 149 149
FT      CARBOHYD 189 189
FT      CARBOHYD 210 210
FT      CARBOHYD 214 214
SQ      SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;
Best Local Similarity 50.7%; Pred. No. 5.9e-40;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY      12 VTKKVEKATVSCGHNSVVEELAQTRIVQKKEKVLTMMSGDNINWEYKNRTIFDITN 71
DB      42 LSKSVKQVLLPCRYNSHDESEDRIVQKHDVLSVINGKLKWEYKNRTIYDNT 100
QY      72 NLSVIYIALRPSDEGTVECVYLKYKDAFKREHLAEVTLVSADPFPPTSIDFELPSNI 131
DB      101 TYSLLIIGLVISDRGYTSCVQKKEKRGTEVKHLALVLSKAPSPNTIESGNPSADT 160
QY      132 RRICSTSGGPEPHLSMLENGEELNAINTVSODETELAVAVSSKLDENMTNHSFCL 191
DB      161 KRITCFASGGPKRFPSFMLENGRELPGINTITISQDESELITISSQDLFNTTRHITKCL 220
QY      192 IKYGLHRYNQTFNNMTTKOEHPDN 216
DB      221 IKYGDHVSDEFTWEKPEDE-PDS 244

RESULT 4
CD86_HUMAN STANDARD; PRT; 329 AA.
ID      CD86_HUMAN
AC      P42081; Q13655;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE      antigen) (CTLA-4 counter-receptor B7.2) (B70) (B063).
GN      CD86 OR CD28LG2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94053735; PubMed=7694363;
RA      Freeman G.J., Gribben J.G., Boussoletis V.A., Ng J.W.,
RA      Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT      "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT      cell proliferation.";

```

RN Science 262:909-911(1993).  
 RN (2)  
 RP SEQUENCE OF 7-329 FROM N.A.  
 RA MEDLINE=94050123; PubMed=7694153;  
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,  
 RA Lanier L.L., Somoza C.,  
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";  
 RT Nature 366:76-79(1993).  
 RN (3)  
 RP SEQUENCE OF 7-329 FROM N.A.  
 RC TISSUE=Forebrain;  
 RA MEDLINE=95331831; PubMed=7541777;  
 RA Jellis C.L., Wang S.S., Remmert P., Borriello F., Sharpe A.H.,  
 RA Green N.R., Gray G.S.,  
 RT "Genomic organization of the gene coding for the costimulatory human  
 RT B-lymphocyte antigen B7-2 (CD86).";  
 RT Immunogenetics 42:85-89(1995).  
 RN (4)  
 RP CHARACTERIZATION.  
 RA MEDLINE=9508403; PubMed=7527824;  
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Lindsay P.S.,  
 RA Okumura K., Ito D., Azuma M.,  
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T  
 RT cell proliferation, cytokine production, and generation of CTL.";  
 RT J. Immunol. 154:97-105(1995).  
 RN (5)  
 RP IDENTIFICATION AS CD86.  
 RA MEDLINE=94348060; PubMed=7520767;  
 RA Engel P., Gribben J.C., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,  
 RA Nadler L.M., Makasa H., Tedder T.F.,  
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and  
 RT activated B lymphocytes is the CD86 differentiation antigen.";  
 RT Blood 84:1402-1407(1994).  
 CC - FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY  
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY  
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,  
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T  
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
 CC - SUBCELLULAR LOCATION: Type I membrane protein.  
 CC - TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND  
 CC MONOCYTES.  
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
 CC - DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".  
 CC -----  
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 CC -----  
 DR EMBL: L25559; AAA58389.1; -  
 DR EMBL: U04343; AAB03814.1; -  
 DR EMBL: U17722; AAA86473.1; -  
 DR EMBL: U17717; AAA86473.1; JOINED.  
 DR EMBL: U17718; AAA86473.1; JOINED.  
 DR EMBL: U17719; AAA86473.1; JOINED.  
 DR EMBL: U17721; AAA86473.1; JOINED.  
 DR MIM: 601020; -  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR SMART: SMO0406; IGV; 1.  
 DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
 KW Receptor.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.  
 FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 248 268 POTENTIAL.  
 FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.  
 FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.  
 FT DISULFID 40 110 POTENTIAL.  
 FT DISULFID 157 218 POTENTIAL.  
 FT CARBOHYD 33 33 POTENTIAL.  
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 27 27 K -> E (TN REF. 3).  
 SQ SEQUENCE 329 AA; 37696 MW; 65DAF6326889CF7D CRC64;  
 Query Match 15.8%; Score 182; DB 1; Length 329;  
 Best Local Similarity 29.0%; Pred. No. 3.3e-08;  
 Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;  
 QY 18 EVATLSC-----GNVSEELAOTRIYQKKKAVLTMM-----SGDMNINPEYNNRTFDI 69  
 DB 34 ETADLPCQGFANSQNSISLELV--VFWDQDENLVLEVYLGEKEKPSVSHKMGRTSFD- 89  
 QY 70 TNNLSIVIALRPSDEGTECVLYKKEKDAFKEHLAEVLTYSKADFPNPSIDFPIPS 129  
 DB 90 SDSWTLRLNLQTKDKGIVOCITHHKKPGRIMIRHOMNSLSLVANSPDEL-----VPS 145  
 QY 130 NTR-----RICTSGGPEPP-RLSMLNGEELNAINTV-----SQDEPELYAVS 175  
 DB 146 NTENYINLTCSISGHGPEPKMSVL-----LRTKNSTLEYDGMQKSDNVTLEYDVS 200  
 QY 176 SKLDF---MWTNHSFMCILKYGHLRV 199  
 DB 201 ISLSVFPDVTSMITFLCILEDTKRL 227  
 RESULT 5  
 ICOL\_HUMAN STANDARD; PRT; 302 AA.  
 AC 075144; O9NR01; Q9HD18;  
 DT 15-OCT-1999 (Rel. 38; Created)  
 DT 15-OCT-2001 (Rel. 40; Last sequence update)  
 DT 01-MAR-2002 (Rel. 41; Last annotation update)  
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-1like protein G150)  
 DE (B7-related protein-1) (B7RP-1)  
 GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP TISSUE=Dendritic cell;  
 RC MEDLINE=20477846; PubMed=11023515;  
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.,  
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds  
 RT ICOS.";  
 RT Blood 96:2808-2813(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
 RC TISSUE=Peripherial blood lymphocytes;  
 RA MEDLINE=20465019; PubMed=11007762;  
 RA Yoshida S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,  
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,  
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.,  
 RT "Characterization of a new human B7-related protein: B7RP-1 is the  
 RT ligand to the co-stimulatory protein ICOS.";  
 RT Int. Immunol. 12:1439-1447(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Leukocyte;

RX MEDLINE-20126021; PubMed-10657606;  
 RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,  
 RA Leonard J.P., Hunter S.E., Zolner R., Thomas J.L., Miyashiro J.S.,  
 RA Jacobs K.A., Collins M.;  
 RT Identification of GL50, a novel B7-like protein that functionally  
 RT binds to ICOS receptor.";  
 RL J. Immunol. 164:1653-1657(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-98403880; PubMed-9734811;  
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,  
 RA Kotani H., Nomura N., Ohara O.;  
 RT Prediction of the coding sequences of unidentified human genes. X.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:169-176(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Ling V., Dunussi-Joannopoulos K.;  
 RT "G150 molecules and uses thereof.";  
 RL Patent number WO0121796, 29-MAR-2001.  
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR  
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND  
 CC CYTOKINE SECRETION. INDICES ALSO B-CELL PROLIFERATION AND  
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN  
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS  
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-  
 CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,  
 CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE  
 CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,  
 CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN  
 CC LYMPH NODES, LEUKOCYTES AND SPLEEN.  
 CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY  
 CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND  
 CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300  
 CC onward for an unknown reason.  
 CC -----  
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 CC -----  
 CC EMBL: AF199028; AAF34739.1; -  
 DR EMBL: AF289028; AAC01176.1; -  
 DR EMBL: AF216749; AAK16241.1; -  
 DR EMBL: AB014553; BAA31628.1; ALT-SEQ.  
 DR EMBL: AX100595; CAC36465.1; -  
 DR MIM: 605717; -  
 DR InterPro: IPR003599; Iq;  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR InterPro: IPR003600; Iq\_Like.  
 DR Pfam: PF00047; Iq; 3.  
 DR SMART: SM00409; Iq; 1.  
 DR SMART: SM00410; Iq\_Like; 1.  
 KW B-cell activation; Immune response; Glycoprotein;  
 KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;  
 KW Alternative splicing.  
 FT SIGNAL 1  
 FT CHAIN 18 POTENTIAL.  
 FT DOMAIN 19 302 ICOS LIGAND.  
 FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).

FT TRANSEM 257 277 POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 278 302 IG-LIKE V-TYPE DOMAIN.  
 FT DOMAIN 30 120 IG-LIKE C2-TYPE DOMAIN.  
 FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.  
 FT DISULFID 37 113 POTENTIAL.  
 FT DISULFID 158 216 POTENTIAL.  
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 300 302 GHV -> ESMNLLILLS (IN ISOFORM 2).  
 SQ SEQUENCE 302 AA; 33349 MW; 647934E21B55E3A4 CRC64;  
 Query Match 14.0%; Score 161; DB 1; Length 302;  
 Best Local Similarity 26.4%; Pred. No. 1,7e-06;  
 Matches 57; Conservative 36; Mismatches 95; Indels 28; Gaps 8;  
 QY 14 KEVKEV---ATLSCG-HNVSVEELAQRIYWO-KEKKVLT---MMSGDMNIMPEYKN 63  
 DB 23 KEVAMGSDVLSGACPEGSFEDNDYVYVWQSEKTVYTHIPONSLENDSKRN 82  
 QY 64 RTIPD---ITNNLSIVTLALPDSDEGTGCVLKYENKAFKREHLAEVTLVKADEPTP 119  
 DB 83 RALMSPAGMLGDSLSRLFNVTYPODEQFHCYLS-QSLGFEVLSYEVTLVHANFVSP 141  
 QY 120 SISDEFTSIRIRICTSGGFEPHLSWLENGEELNAITVYSODETE-----L 171  
 DB 142 VVSAPHSPSODELFTFCISINGPRPNVYINKKD---NSLDOALQNDTVFLMGRGL 196  
 QY 172 YAVSKLDENMTNHSFCLIKYGLRVNQTENNMT 207  
 DB 197 YDVVSVLRIARTPSVNICCIENVLQONLTVGSQT 232  
 RESULT 6  
 ID CD86\_MOUSE STANDARD; PRT; 309 AA.  
 AC P42082;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE T lymphocyte activation antigen CD86 precursor (Activation B7-2  
 DE antigen) (Early T cell costimulatory molecule-1) (Etc-1).  
 GN CD86.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94065585; PubMed-7504059;  
 RA Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,  
 RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,  
 RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;  
 RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates  
 RT T cell proliferation and interleukin 2 production.";  
 RL J. Exp. Med. 178:2185-2192(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129;  
 RX MEDLINE-96094437; PubMed-7499829;  
 RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;  
 RT "Differential expression of alternate mB7-2 transcripts.";  
 RL J. Immunol. 155:3490-3497(1995).  
 RN [3]  
 RP SEQUENCE OF 7-309 FROM N.A.  
 RX MEDLINE-94230971; PubMed-7513726;  
 RA Chen C., Gault A., Shen L., Nabavi N.;  
 RT "Molecular cloning and expression of early T cell costimulatory  
 RT molecule-1 and its characterization as B7-2 molecule.";  
 RL J. Immunol. 152:4929-4936(1994).  
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL



CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN  
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS  
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-  
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION  
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE  
 CC TH2 PHENOTYPE.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID  
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES  
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY  
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S  
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY  
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,  
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-  
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF  
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.  
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYOGENESIS; IN THE YOLK  
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT  
 CC 14.5 DPC.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
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 CC -----  
 CC DR EMBL: AF216747; AAF45149.1; -  
 CC DR EMBL: AF199027; AAF4738.1; -  
 CC DR EMBL: AX100593; CAC36463.1; -  
 CC DR EMBL: AX100593; CAC36464.1; -  
 CC DR EMBL: AE394451; AAK7544.1; -  
 CC DR MGD: MG1:1354701; Icosl.  
 CC DR InterPro: IPR003599; Ig.  
 CC DR InterPro: IPR003006; Ig\_MHC.  
 CC DR InterPro: IPR003600; Ig\_Like.  
 CC DR Pfam: PF00047; Ig\_1.  
 CC DR SMART: SM00409; Ig\_1.  
 CC DR SMART: SM00410; Ig\_Like; 1.  
 CC KM B-cell activation; Immune response; Glycoprotein;  
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;  
 CC Alternative splicing.  
 CC KW SIGNAL 46  
 CC FT CHAIN 1  
 CC FT DOMAIN 47 322  
 CC FT TRANSMEM 278 298  
 CC FT DOMAIN 299 322  
 CC FT DOMAIN 55 145  
 CC FT DOMAIN 178 250  
 CC FT DOMAIN 31 38  
 CC FT DOMAIN 289 292  
 CC FT DISULFID 62 138  
 CC FT DISULFID 185 243  
 CC FT CARBOHYD 71 71  
 CC FT CARBOHYD 120 120  
 CC FT CARBOHYD 163 163  
 CC FT CARBOHYD 200 200  
 CC FT CARBOHYD 213 213  
 CC FT CARBOHYD 252 252  
 CC FT CARBOHYD 265 265  
 CC FT VARSPLIC 321 322  
 CC FT CONFLICT 237 237  
 CC FT SEQUENCE 322 AA; 35960 MW; 55CBA4AD12E47B6 CRC64;  
 CC Query Match 13.1%; Score 150.5; DB 1; Length 322;

Best Local Similarity 27.1%; Pred. No. 1.4e-05;  
 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;  
 QY 2 LSHCC--SGVHIVKEKEVATLSCGNVSYE-----ELAQRIYOKERKMV-----L 48  
 Db 38 LSLCAASAEIEVGAMGNSVNLSC-----IDPRRHRLNLSGLVYWMQIENPEVSVYYL 92  
 QY 49 TMASGDANIMEEYKRNRTFDITN---NLSTVIALRSDSGTECYVLAKEKNAFKREH 104  
 Db 93 PYKSPGINVDSYKRNKRLSLDSMKGNFSLKKNVTPDQOETCRV--FMNATLTVK 150  
 QY 105 LAE--VTLTVKADPPTP--SISDEIFPSNIRRICSTSGGFPEPHLSWLENGELMAIN 160  
 Db 151 ILEEVRLRVAANSTPYTISDSNSNGOE--RTYCKSKNRYPEPNLXVI--NTDNSLSD 208  
 QY 161 TTYSODP---ETELVAVSSKLDFENMTNHSFCLIKYGLHVN-----QTFNMNTTK 209  
 Db 209 TALQNNFYVYLLKGLDYVISTLRPLWTSRGVLDCEVNAVLHQNITSISQSEFTGNNTK 268  
 RESULT 8  
 CD86\_RABIT STANDARD; PRT; 330 AA.  
 ID CD86\_RABIT  
 AC P42071;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 41, Last annotation update)  
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2  
 DE antigen).  
 GN CD86.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B/J X CHB; HM;  
 RX MEDLINE=95369849; PubMed=7642234;  
 RA Isono T., Seto A.;  
 RT "Cloning and sequencing of the rabbit gene encoding T-cell  
 RT costimulatory molecules.";  
 RL Immunogenetics 42:217-220(1995).  
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY  
 CC BINDING OF CD28 OR CTLA-4, MAY PLAY A CRITICAL ROLE IN THE EARLY  
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.  
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T  
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
 CC -----  
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 CC -----  
 CC DR EMBL: D49842; BAA08642.1; -  
 CC DR InterPro: IPR003006; Ig\_MHC.  
 CC DR InterPro: IPR003596; Ig\_V.  
 CC DR SMART: SM00406; Igy; 1.  
 CC DR PROSITE: PS00290; Ig\_MHC; 1.  
 CC KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
 CC Receptor.  
 CC FT SIGNAL 1 22  
 CC FT CHAIN 23 330  
 CC FT DOMAIN 23 247  
 CC FT TRANSMEM 248 268  
 CC FT DOMAIN 269 330  
 CC B LYMPHOCYTE ACTIVATION ANTIGEN CD86.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).

```

FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 149 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;

Query Match 12.2%; Score 140.5; DB 1; Length 330;
Best Local Similarity 27.4%; Pred. No. 9.8e-05;
Matches 60; Conservative 34; Mismatches 84; Indels 41; Gaps 12;

OY 18 EVATLSGSH-NVSEVLEAOTRIYOKREKMYLTM-----SGDMNIWPEYKRTIFDITN- 71
DB 34 KTRDLPCOFNFSOSRSLSELVEMQDERLVLYELFGREKPDVDPKXRTISFDSQSW 93
OY 72 NLSIVIALRPDEGTVECVLYLKEKAFREHLAEVTLSSKADFPFPIISDFEIPISNI 131
DB 94 NQLHNVQIK--DKGVYQCFVHRGAKGLPIYQMSELSTLANFTQPEIT-----LISNI 147
OY 132 RR-----IICSTSGGFEPEPLSLWENGELNAINITV-----SDDPELEY--AVSS 176
DB 148 TRSAINLTCCSSVQGYEPKMKFF---VLKTEATTEYGVIEKSDQNVGLYNISISG 203
OY 177 KLDF-NMTNHSFMCILIKYGLHVNQFMNTTKOEHP 214
DB 204 SITFSDDIRNATITCYV-----QTESITYSQ-HFP 233

RESULT 9
C166_MOUSE STANDARD; PRT; 583 AA.
ID C166_MOUSE 070136;
AC 061490: 070136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM) (DM-GRASP protein).
GN ALCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NS.
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajgorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA Kobarg J., Starling G.C., Sladko A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs and mediates cross-species binding.";
RL Eur. J. Immunol. 27:1469-1478(1997).

[2]
RN SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse.";
RL J. Neurobiol. 25:831-845(1994).

-1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.

```

```

CC -1- SIMILARITY: CONTAINS 3 IMMUGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUGLOBULIN-LIKE V-TYPE DOMAINS.
-----
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DR EMBL: U95030; AAC06342.1; -
DR EMBL: L25274; AAA37528.1; -.
DR HSSP: Q13740; 1KTC.
DR MGI: MGI:1313266; ALCAM.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; Ig; 3.
DR SMART: SM00410; Ig_Like; 2.
DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 583
FT DOMAIN 28 527
FT TRANSMEM 528 549
FT DOMAIN 550 583
FT DOMAIN 263 321
FT DOMAIN 347 399
FT DOMAIN 428 492
FT DISULFID 43 113
FT DISULFID 157 220
FT DISULFID 270 313
FT DISULFID 354 392
FT DISULFID 435 485
FT CARBOHYD 95 95
FT CARBOHYD 167 167
FT CARBOHYD 265 265
FT CARBOHYD 306 306
FT CARBOHYD 361 361
FT CARBOHYD 457 457
FT CARBOHYD 480 480
FT CARBOHYD 499 499
FT CONFLICT 227 232
FT CONFLICT 454 454
SO SEQUENCE 583 AA; 65161 MW; E7BAF8FCA8F9489 CRC64;

Query Match 11.7%; Score 134.5; DB 1; Length 583;
Best Local Similarity 25.2%; Pred. No. 0.00063;
Matches 38; Conservative 34; Mismatches 54; Indels 25; Gaps 7;

OY 59 PEYNKRTIFDTNNISYIALRPDEGTVECVLYLKEKADARKREHLAEVTLSSKADFPPT 118
DB 84 PEYKDR--LSSEYNTLSIAKSIDERKFCYMLVT-EDNVEAPLVVY-----FKQ 133

OY 119 PSIDFE-----IPSNRRI-ICSTSGGFEPEPLSLWENGELNAINITVS-----QD 166
DB 134 PSKEIYVAKAFLETDQKKLDCISRDSYFPGNITWIRNGKVLQVPEGEVALFKKEID 193

OY 167 PETELIYAVSSKLDFNMTNNH---SEFMCLIKY 194
DB 194 PGQLTYVTSLEKTKTRSDIQMPFTCSVTY 224

RESULT 10
C166_HUMAN STANDARD; PRT; 583 AA.
ID C166_HUMAN 013740: 060892;
AC 013740: 060892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

```

DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)  
 (ALCAM).  
 GN ALCAM OR MEMD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95279947; PubMed=7760007;  
 RA Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,  
 Wang W.-C., Margardt H., Neubauer M., Pesando J.M., Francke U.,  
 Haynes B.F., Aruffo A.;  
 RT "Cloning, mapping, and characterization of activated leukocyte-cell  
 adhesion molecule (ALCAM), a CD6 ligand.";  
 RL J. Exp. Med. 181:2213-2220(1995).  
 RN [2]  
 RP SEQUENCE OF 2-583 FROM N.A.  
 RX MEDLINE=98161527; PubMed=9502422;  
 RA Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,  
 van Kooyk Y., Bloemers H.P., Swart G.W.;  
 RT "MEM, a new cell adhesion molecule in metastasizing human melanoma  
 cell lines, is identical to ALCAM (activated leukocyte cell adhesion  
 molecule).";  
 RL Am. J. Pathol. 152:805-813(1998).  
 RN [3]  
 RP CD6-BINDING DOMAINS.  
 RX MEDLINE=96420463; PubMed=8823162;  
 RA Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;  
 RT "Recognition of diverse proteins by members of the immunoglobulin  
 superfamily: delineation of the receptor binding site in the human  
 CD6 ligand ALCAM.";  
 RL Biochemistry 35:12287-12291(1996).  
 RN [4]  
 RP 3D-STRUCTURE MODELING OF 28-133.  
 RX MEDLINE=96060095; PubMed=8520490;  
 RA Bajorath J., Bowen M.A., Aruffo A.;  
 RT "Molecular model of the N-terminal receptor-binding domain of the  
 human CD6 ligand ALCAM.";  
 RL Protein Sci. 4:1644-1647(1995).  
 CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN  
 NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC  
 INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO  
 ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF  
 THE NERVOUS SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.  
 CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD166 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd166.htm".  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L38608; AAB59499.1; -;  
 DR EMBL: Y10183; CAA71256.1; -;  
 DR PDB: 1KJC; 03-APR-96.  
 DR MIM: 601662; -;  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR Pfam: PF00047; Ig; 5.  
 DR SMART: SMO0409; Ig; 2.  
 DR SMART: SMO0410; Ig\_Like; 2.  
 DR PROSITE: PS00290; Ig\_MHC; FALSE\_NEG.  
 KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;  
 Repeat; Signal; 3D-structure; Polymorphism.

FT SIGNAL 1 27  
 FT CHAIN 28 583  
 FT DOMAIN 28 527  
 FT TRANSMEM 528 549  
 FT DOMAIN 550 583  
 FT DOMAIN 36 120  
 FT DOMAIN 150 227  
 FT DOMAIN 263 321  
 FT DOMAIN 347 399  
 FT DOMAIN 428 492  
 FT DISULFID 43 113  
 FT DISULFID 157 220  
 FT DISULFID 270 313  
 FT DISULFID 354 392  
 FT DISULFID 435 485  
 FT CARBOHYD 91 91  
 FT CARBOHYD 95 95  
 FT CARBOHYD 167 167  
 FT CARBOHYD 265 265  
 FT CARBOHYD 306 306  
 FT CARBOHYD 361 361  
 FT CARBOHYD 457 457  
 FT CARBOHYD 480 480  
 FT CARBOHYD 499 499  
 FT VARIANT 258 258  
 FT VARIANT 301 301  
 FT VARIANT 301 301  
 FT VARIANT M->T.  
 FT VARIANT /FTID=VAR\_003907.  
 FT VARIANT M->T.  
 FT VARIANT /FTID=VAR\_003908.  
 FT VARIANT E023FB3974A60284 CRC64;  
 SQ SEQUENCE 583 AA; 65132 MW; /FTID=VAR\_003908.  
 Query Match 11.6%; Score 133.5; DB 1; Length 583;  
 Best Local Similarity 24.5%; Pred. No. 0.00077;  
 Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;  
 QY 59 PEYKRTTFDTNNLSIVLALRPSDEGTVCVLYLKYKDAFKRHLAEVLSVKADEPT 118  
 Db 84 PEYKDR--LNLSSENTLSISNARISDEKRFVOMLVY-EDVFEAPTYKV-----FKQ 133  
 QY 119 PSISDFE-----IPSNIRI-ICSTSGFPEPHSMLENEELNATVY-----SQD 166  
 Db 134 PSKEPIYKALFLETEQKLDGDCISEDSYDGNITWRNGKVLPLGAVVITFKKMD 193  
 QY 167 PETELYAVSSKIDENMT---TNHSEFCLIKY 194  
 Db 194 PVTOLYMTSTLEYTKTKADIDMPTCSVY 224  
 RESULT 11  
 ID BRFL\_EBV STANDARD; PRT; 221 AA.  
 AC P03228;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE 33 kDa early protein (P33).  
 GN BARFL.  
 OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Lymphocryptovirus.  
 ON NCBI\_TaxID=10377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84270667; PubMed=6087149;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,  
 Tufnell P.S., Watliff B.G.;  
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
 RL Nature 310:207-211(1984).  
 RN [2]  
 RP IDENTIFICATION OF PROTEIN.  
 RX MEDLINE=90059873; PubMed=2555151;  
 RA Wei M.X., Ooka T.;  
 RT "A transforming function of the BARFL gene encoded by Epstein-Barr

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RT virus."
RL EMBO J. 8:2897-2903(1989).
CC -1- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC -----
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CC -----
DR EMBL; V01555; CAA24809.1; -.
DR PIR; A03792; QOBE48.
DR PIR; S33058; S33058.
DR InterPro: IPR003600; IG_1like.
DR SMART; SM00410; IG_1like; 1.
KW Early protein; Oncogene.
SQ SEQUENCE 221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match
Best Local Similarity 11.2%; Score 129; DB 1; Length 221;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSEELAQTRIMOK-----EKKMVLTMMSGDMNIMPE 60
DB 19 QAVTAFLEGEVTLTS-----YMRVSLGPELEVSWEKLGEGEVLGRMHHDV-IFLE 71
QY 61 YKNTIFDI---TNNSIVILALRPSDEGTCECVLKEKAFKREHLEAV--TLV-- 112
DB 72 WPRRGFDHRSATFPLVYTAANISHDGNLCKRMKLGFEVTKOEHLSVVKPLTSLVSHS 131
QY 113 -KADFPPIISDEPIPTSNIRRICSTSGGPPPEHLSWL 150
DB 132 ERSGFP-----DFSVLT-----VTCTVNAFPHPHVOML 159

RESULT 12
BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTN1A1 OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human butyrophilin reveals a
RT potential receptor function."
RL Biochim. Biophys. Acta 1306:1-4(1996).
CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC -----
DR EMBL; U39576; AAC50489.1; -.
DR MIM; 601610; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
DR Pfam; PF00047; 1g; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00406; 1GV; 1.
DR SMART; SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 27
FT DOMAIN 27
FT TRANSMEM 243
FT DOMAIN 270
FT CARBOHYD 55
FT CARBOHYD 215
SQ SEQUENCE 526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match
Best Local Similarity 11.1%; Score 127; DB 1; Length 526;
Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSEELAQTRIMOKKKKVLTMMSG---DMNTPEYKNTIF-- 67
DB 42 VEGDALPRLSPNASEAHL-ELRWRKRVSPAVLVHRDGRQEAQMPYRGKATLVQD 100
QY 68 -DITNLSIVILALRPSDEGTCECVLKEKAFKREHLEAVLSVADPTPSISPEI 126
DB 101 GIAGKRVALARIGKRVSDGECTCF---FREDSTYELAL-VHLKVAALGSDPHIS-MQV 154
QY 127 PPSNIRRICSTSGGPPPEHLSW-LENGEELNAINTVSODPETE-LYAVSKLDPMNT 184
DB 155 QENGETICECTSGVWPBPVOVWRTSKGEKFP--STSESINPDEGLFTYAAVYITDTS 212
QY 185 NNSFMCILK 193
DB 213 TKNVSCYIQ 221

RESULT 13
C166_CHICK STANDARD; PRT; 588 AA.
ID C166_CHICK
AC P42292;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CD166 antigen precursor (SCI glycoprotein) (BEN glycoprotein) (DM-
DE GRASP protein) (UC7 protein).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 34-53.
RC TISSUE=Embryo;
RX MEDLINE=92030150; PubMed=1931049;
RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RT "Molecular cloning and expression of a novel adhesion molecule, SCI."
RL Neuron 7:535-545(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91373449; PubMed=1873027;
RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA Chang S.;

```



RT "DM-CRASP, a novel immunoglobulin superfamily axonal surface protein  
RT that supports neurite extension.";  
RT Neuron 7:209-220(1991).  
RN (3)  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.  
RC TISSUE-Bursa of fabricius;  
RA MEDLINE=92302224; PubMed=1608932;  
RA Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;  
RT "BEN, a surface glycoprotein of the immunoglobulin superfamily, is  
RT expressed in a variety of developing systems.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).  
RN [4]  
RP POSSIBLE FUNCTION.  
RX MEDLINE=92211411; PubMed=1313497;  
RA Pourquie O., Halinon M.E.R., le Douarin N.M.;  
RT "Association of BEN glycoprotein expression with climbing fiber  
RT axogenesis in the avian cerebellum.";  
RL J. Neurosci. 12:1548-1557(1992).  
CC -1- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING  
CC FIBER AXONOGEMESIS. SUPPORTS NEURITE EXTENSION.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.  
CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL  
CC FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTORNEURONS. FOUND IN  
CC EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH  
CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS  
CC OF BEN.  
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC  
CC DEVELOPMENT.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; S63276; AAB20170.1; -  
DR EMBL; M76678; AAA48602.1; -  
DR EMBL; X64301; CAA45579.1; -  
DR HSSP; Q13740; 1KIC.  
DR InterPro; IPR003559; Ig.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00409; Ig\_3.  
DR SMART; SM00410; Ig\_Like\_2.  
DR PROSITE; PS00290; IG\_MHC; FALSE\_NEG.  
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;  
KW Repeat; Signal.  
FT SIGNAL 1 33  
FT CHAIN 34 588 CD166 ANTIGEN.  
FT DOMAIN 34 532 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 533 533 POTENTIAL.  
FT DOMAIN 534 588 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 42 126 IG-LIKE V-TYPE DOMAIN 1.  
FT DOMAIN 156 233 IG-LIKE V-TYPE DOMAIN 2.  
FT DOMAIN 269 326 IG-LIKE C2-TYPE DOMAIN 1.  
FT DOMAIN 352 404 IG-LIKE C2-TYPE DOMAIN 2.  
FT DOMAIN 433 497 IG-LIKE C2-TYPE DOMAIN 3.  
FT DISULFID 49 119 POTENTIAL.  
FT DISULFID 163 226 POTENTIAL.  
FT DISULFID 276 319 POTENTIAL.  
FT DISULFID 359 397 POTENTIAL.  
FT DISULFID 440 490 POTENTIAL.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT -----

FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 504 504 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 2 10 MERRAAR -> EPPRRRP (IN REF. 3).  
FT CONFLICT 25 25 A -> S (IN REF. 3).  
FT CONFLICT 112 113 SD -> R (IN REF. 3).  
FT CONFLICT 329 329 A -> T (IN REF. 2).  
FT CONFLICT 401 402 LQ -> HK (IN REF. 2).  
SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;  
  
Query Match 10.7%; Score 122.5; DB 1; Length 588;  
Best Local Similarity 25.7%; Pred. No. 0.0064;  
Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;  
  
QY 59 PEYKRTITFDTNLNLIVIALRPSDEGTVCVYLKKEKDAFKREHLAEVTLVSKADPEPT 118  
DQ 90 PDYKDR--LSISENTYTLSTKNARISDEKRFVCMVLT--EDDYSEPTVYKV-----FKQ 139  
DQ 119 PS-----ISDFEIPTSNIRI-ICSTSGGFPEPHLSWLENG-----EELNAINTVSQ 165  
DQ 140 PSCPEILHQADF-LETERKLKMGECVVDSDYSGNVTWYKNGRVILQPEVEVYINLRKVE 198  
QY 166 DPEELAVVSKLDPNMT--TNSFPCILKY 194  
DQ 199 NSTGLFTMTSLQYMPTEKDNAKFTCIYVY 230  
  
RESULT 14  
BUTY\_MOUSE STANDARD; PRT; 524 AA.  
ID BUTY\_MOUSE  
AC Q62356; P97392;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Butyrophilin precursor (BT).  
GN PBN1AL OR PBN1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Mammary gland;  
RX MEDLINE=97148936; PubMed=8955761;  
RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;  
RT "Structural organization and mammary-specific expression of the  
RT butyrophilin gene.";  
RL Mamm. Genome 7:900-905(1996).  
RN [2]  
RP SEQUENCE OF 39-487 FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=96125722; PubMed=8541302;  
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;  
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin  
RT specifically associates with a 150-kDa protein of mammary epithelial  
RL cells and milk fat globule membrane.";  
RL Biochim. Biophys. Acta 1245:285-292(1995).  
CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT  
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE  
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA  
CC MEMBRANE (BY SIMILARITY).  
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN  
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF  
CC PREGNANCY AND IS MAXIMAL DURING LACTATION.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOS  
CC SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.  
CC -----



FT VARSPLIC 804 1049 MISSING (IN ISOFORM N-CAM 140).  
SQ SEQUENCE 1088 AA; 117778 MW; 62738B5B03F3E83 CRC64;  
Query Match 10.1%; Score 116.5; DB 1; Length 1088;  
Best Local Similarity 24.0%; Pred. No. 0.044;  
Matches 43; Conservative 31; Mismatches 58; Indels 47; Gaps 9;  
QY 18 EVATLSCGHNVSEELAQRTIYWQEKKKVLTMMSGDMIMPEYKNTTFDITNNLSIVI 77  
DB 130 EDVAVIICDVSSSIPSI---ITWRHKGDVI-----FKDVRFVLANNYLQI 173  
QY 78 LALRPSDEGTYYECVVLKYEKDAFKREHLAEVTLVSKADFPPTPSISDEI---PTSNIR- 133  
DB 174 RGIKKTDEGTIRC-----EGRIIARGEINIKDIQIVYNP-PTIQARQLRVNATANMAES 227  
QY 134 -IICSTSGGFPEPHLSWLENGEELNAINITVSDPETELYAVSSKLDEN---MTTNH 186  
DB 228 VVLSCDADGFPDPEISWIKKGEP-----EDGE-----EKISFNEDQSEMTIHH 271

Search completed: October 17, 2002, 16:36:54  
Job time : 15 secs





QY 122 SDFEIPISNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 181  
 Db 148 TDFEIPPSNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 207  
 QY 182 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 216  
 Db 208 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 242

RESULT 2  
 Q28499 PRELIMINARY; PRT; 288 AA.  
 AC 028499;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE B7 PROTEIN (CD80 PROTEIN PRECURSOR).  
 GN B7 OR N939.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing and homology analysis of nonhuman primate  
 Fas/Fas-Ligand and co-stimulatory molecules.";  
 RL Immunogenetics 0:0-0(2001).  
 DR EMBL: U19840; AAA86706.1; -.  
 DR EMBL: AF344849; AAK37609.1; -.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00409; Ig\_1.  
 DR SMART: SM00410; IG\_Like; 1.  
 KW Signal.  
 FT SIGNAL.  
 SO SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;  
 Best Local Similarity 96.3%; Pred. No. 2.2e-94;  
 Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVEKVAATLSCGHNVSVEELAQTRITVQKKEKMYLTMMSGDMNTWPEY 61  
 Db 28 LSHFCGVIHVTKEVEKVAATLSCGHNVSVEELAQTRITVQKKEKMYLTMMSGDMNTWPEY 87  
 QY 62 KNRTIFDITNNLSVILALRPSDEGTGECVILKYEKDAFKREHLAEVTLVSKADFPPTSI 121  
 Db 88 KNRTIFDITNNLSVILALRPSDEGTGECVILKYEKDAFKREHLAEVTLVSKADFPPTSI 147  
 QY 122 SDFEIPISNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 181  
 Db 148 TDFEIPPSNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 207  
 QY 182 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 216  
 Db 208 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 242

RESULT 3  
 Q9BDN6

ID 09BDN6 PRELIMINARY; PRT; 288 AA.  
 AC 09BDN6;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CD80 PROTEIN.  
 GN NMB71.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Cercopithecus.  
 OX NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-Ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL: AF344839; AAK37535.1; -.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00409; Ig\_1.  
 DR SMART: SM00410; IG\_Like; 1.  
 SO SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;  
 Best Local Similarity 95.3%; Pred. No. 5.4e-93;  
 Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVEKVAATLSCGHNVSVEELAQTRITVQKKEKMYLTMMSGDMNTWPEY 61  
 Db 28 LSHFCGVIHVTKEVEKVAATLSCGHNVSVEELAQTRITVQKKEKMYLTMMSGDMNTWPEY 87  
 QY 62 KNRTIFDITNNLSVILALRPSDEGTGECVILKYEKDAFKREHLAEVTLVSKADFPPTSI 121  
 Db 88 KNRTIFDITNNLSVILALRPSDEGTGECVILKYEKDAFKREHLAEVTLVSKADFPPTSI 147  
 QY 122 SDFEIPISNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 181  
 Db 148 TDFEIPPSNIRRICSTGGFPEPHLSWLENGEELNAINTVSODPETELTVAVSSKLDNF 207  
 QY 182 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 216  
 Db 208 MTNHSFMCILIKYGHILRVNQTFFNMNTPKQEHFPDN 242

RESULT 4  
 Q28347 PRELIMINARY; PRT; 289 AA.  
 AC 028347;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE B7 PROTEIN (FRAGMENT).  
 GN B7.  
 OS Cercopithecus torquatus (red-crowned mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Cercopithecus.  
 OX NCBI\_TaxID=9530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).  
 DR EMBL: U19833; AAA86700.1; -.

DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00410; Ig\_Like; 2.  
 FT NON\_TER 289  
 SO SEQUENCE 289 AA; 33030 MW; 5ED6A3F6A3C59297 CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 289;  
 Best Local Similarity 95.3%; Pred. No. 5.4e-93;  
 Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 61  
 DB 28 LSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 87  
 QY 62 KNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 121  
 DB 88 KNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 147  
 QY 122 SDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDFN 181  
 DB 148 TDFEIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDFN 207  
 QY 182 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 216  
 DB 208 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 242

## RESULT 5

ID Q9N2I3 PRELIMINARY; PRT; 230 AA.  
 AC Q9N2I3;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CD80 PROTEIN PRECURSOR.  
 GN CD80/B7.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LANDRACE; TISSUE=SPLEEN;  
 RA Wada M., Amoe S., Hoshi M., Nio M., Ohi R.;  
 RT "Porcine CD80(B-7) mRNA, partial cds."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB026121; BAA90700.2; -  
 DR InterPro: IPR003599; Ig\_  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART: SM00409; Ig; 1.  
 DR SMART: SM00410; Ig\_Like; 1.  
 KW Signal.  
 FT CHAIN 1 29 POTENTIAL.  
 FT SEQUENCE 30 230 POTENTIAL.  
 SO SEQUENCE 230 AA; 26028 MW; EB63AD172663C444 CRC64;

Query Match 66.5%; Score 764; DB 6; Length 230;  
 Best Local Similarity 67.0%; Pred. No. 3e-63;  
 Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 1 GLSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 60  
 DB 22 GLSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 81  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 120  
 DB 82 YENKFTFDTNNLCIVIALRLSDNGITTCVYQKREKRSYKLEHLTSVKLMWKAQFPVPS 141  
 QY 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDF 180  
 DB 148 TDFEIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDF 207

DB 142 ITALGNPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDF 201  
 QY 181 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 216  
 DB 202 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 242

Query Match 94.4%; Score 1085; DB 6; Length 289;  
 Best Local Similarity 95.3%; Pred. No. 5.4e-93;  
 Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 61  
 DB 28 LSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 87  
 QY 62 KNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 121  
 DB 88 KNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 147  
 QY 122 SDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDFN 181  
 DB 148 TDFEIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDFN 207  
 QY 182 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 216  
 DB 208 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 242

Query Match 66.5%; Score 764; DB 6; Length 230;  
 Best Local Similarity 67.0%; Pred. No. 3e-63;  
 Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 1 GLSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 60  
 DB 22 GLSHFSCSVIHVTEKVEKVALSCGHNVSEELAQTRITYOKEKKMVLTMNSGDMNIPPEY 81  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTCECVYLKFKREHLAEVTLGVKADFPPTSI 120  
 DB 82 YENKFTFDTNNLCIVIALRLSDNGITTCVYQKREKRSYKLEHLTSVKLMWKAQFPVPS 141  
 QY 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDF 180  
 DB 142 ITALGNPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSODPETELAYVSSKIDF 201  
 QY 181 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 216  
 DB 202 MTNHSFMCILIKYGHLEVNQTFNNNTKQEHFDPN 242

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LANDRACE; TISSUE-ILEUM MUCCOSA;  
 RA Wada M., Amai S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,  
 RT Hayashi Y., Ohl R.;  
 RT Cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble  
 RT isoforms.  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB049760; BAB40952.1;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00410; IG\_Like; 1.  
 KW Signal.  
 FT CHAIN 30 297  
 SQ SEQUENCE 297 AA; 33438 MW; 23109711EA63EF23 CRC64;

Query Match 66.4%; Score 762.5; DB 6; Length 297;  
 Best Local Similarity 66.5%; Pred. No. 5,8e-63;  
 Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

OY 1 GLSHFGSGVIHTKEVEVATLSCGHNVSVEELAQRTIYQKKEKAVLTMSGDMNIMPE 60  
 DB 22 GLFDFGSGIIVQTKYKEIVLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 81  
 OY 61 YKNRTTFDITNNLSIVTLALRPSDEGTGECVLYKEKDAFKREHLAEVLTSLKADFPPTS 120  
 DB 82 YENRTFTDVTNNLCIVTLALRLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 141  
 OY 121 ISDFELPTSNIRKICSTSGGPEPHLSWLENGEELNATNTVSODEPELYAVSSKLD 180  
 DB 142 ITALGNPSPNIRKICSTSGGPEPHLSWLENGEELNATNTVSODEPELYAVSSKLD 201  
 OY 181 NMTNHSFMCILKYGHRLVNOTFNW-NITKOE 211  
 DB 202 NVTGNHSMFLVKGGLVTSQTFNWKSAKRE 233

RESULT 8  
 O9TT71 PRELIMINARY; PRT; 229 AA.

AC O9TT71  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CD80 PROTEIN PRECURSOR.  
 GN CD80 OR CD80/B7-1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Paas S.J., Giannoni M.A., Mickle A., Klesecker C.L., Reed D.J., Wu D.,  
 RA Foodor W.L., Meuller J.P., Matis L.A., Rother R.P.;  
 RT "Primary Structure and Functional Characterization of a Soluble,  
 RT Alternatively Spliced Form of B7-1."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SPLEEN;  
 RA Wada M., Amai S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,  
 RT Ohl R.;  
 RT "Splicing Isoform of Porcine CD80."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF203442; BAA22749.1;  
 DR EMBL; AB038153; BAA90764.1;  
 DR InterPro; IPR003599; Ig.

DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00410; IG\_Like; 1.  
 KW Signal.  
 FT CHAIN 30 229  
 SQ SEQUENCE 229 AA; 25900 MW; C3AD17263634A4ED CRC64;

Query Match 66.2%; Score 761; DB 6; Length 229;  
 Best Local Similarity 67.8%; Pred. No. 5,7e-63;  
 Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;

OY 1 GLSHFGSGVIHTKEVEVATLSCGHNVSVEELAQRTIYQKKEKAVLTMSGDMNIMPE 60  
 DB 22 GLFDFGSGIIVQTKYKEIVLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 81  
 OY 61 YKNRTTFDITNNLSIVTLALRPSDEGTGECVLYKEKDAFKREHLAEVLTSLKADFPPTS 120  
 DB 82 YENRTFTDVTNNLCIVTLALRLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 141  
 OY 121 ISDFELPTSNIRKICSTSGGPEPHLSWLENGEELNATNTVSODEPELYAVSSKLD 180  
 DB 142 ITALGNPSPNIRKICSTSGGPEPHLSWLENGEELNATNTVSODEPELYAVSSKLD 201  
 OY 181 NMTNHSFMCILKYGHRLVNOTFNW 205  
 DB 202 NVTGNHSMFLVKGGLVTSQTFNWK 226

RESULT 9  
 O9GMZ8 PRELIMINARY; PRT; 292 AA.

AC O9GMZ8  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE B-LYMPHOCYTE ACTIVATION ANTIGEN B7-1 (CD80).  
 GN CD80.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 NCBI\_TaxID=9685;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20485322; PubMed=11029611;  
 RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,  
 RA Izumiyama Y., Ikeda Y., Mikami T., Takahashi E.;  
 RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte  
 RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which  
 RT interact with human CTLA4-1g."  
 RL Eur. J. Immunogenet. 27:427-430 (2000).  
 DR EMBL; AB030651; BAB11687.1;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00410; IG\_Like; 2.  
 SQ SEQUENCE 292 AA; 33540 MW; ED9AECE10D30401 CRC64;

Query Match 64.7%; Score 743; DB 6; Length 292;  
 Best Local Similarity 63.3%; Pred. No. 3,7e-61;  
 Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

OY 2 LSHPGSGVIHTKEVEVATLSCGHNVSVEELAQRTIYQKKEKAVLTMSGDMNIMPE 61  
 DB 28 LEFPGSGIIVQTKYKEIVLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 87  
 OY 62 KNRITFTDITNNLSIVTLALRPSDEGTGECVLYKEKDAFKREHLAEVLTSLKADFPPTS 121  
 DB 88 KNRITFTDITNNLSIVTLALRLSDNGTYTCVQKREKSGYKLEHLTVKLVKADFPVPS 147





Matches 134; Conservative 28; Mismatches 47; Indels 3; Gaps 2;

```

QY 1 GLSHFCGVI--HYTKVEKVALSCGHNVSEBELAOTRIYQEKKMYLTMMGDMNIM 58
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 27 GLFYFCGIIQVKNKYKVEKVALSCDYNSTTELMKRYIWKQKDEVLAVYSGOTKWSKY 86
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 59 PEKKNRTIPDITNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFP 117
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 87 PEKKNRTIPDITNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFP 146
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 118 TPEISFEIPTNSIRRICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSK 177
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 147 VPTINDLGNPSPIRRLICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSK 206
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 178 LDFNMTNHSFCLIKYGHILRVNQTENMTTK 209
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 207 LDFNMTNHSFCLIKYGHILRVNQTENMTTK 238
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

## RESULT 13

```

ID 09TOS8 PRELIMINARY; PRT; 235 AA.
AC 09TOS8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SECRETED B7-1 PROTEIN PRECURSOR.
GN CD80.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106825; AAF17296.1; -.
DR EMBL; AF106831; AAF17296.1; -.
DR EMBL; AF106829; AAF17294.1; JOINED.
DR EMBL; AF106830; AAF17294.1; JOINED.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_1.
DR SMART; SM00410; IG_Like; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SO SEQUENCE 235 AA; 26917 MW; CC08CAA676BC40A CRC64;

```

Query Match 61.4%; Score 705; DB 6; Length 235;  
 Best Local Similarity 61.5%; Pred. No. 9,7e-58;  
 Matches 128; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

```

QY 2 LSHFCGVIHYTKVEKVALSCGHNVSEBELAOTRIYQEKKMYLTMMGDMNIMPEY 61
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 28 LEFYFCGIIQVKNKYKVEKVALSCDYNSTTELMKRYIWKQKDEVLAVYSGOTKWSKY 87
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 62 KNRITFDITNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFPPTSI 121
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 88 ENRTFADFTNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFPPTSI 147
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 122 SDFEITPSNIRRICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSKLDEN 181
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 148 TDLGNPSPIRRLICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSKLDEN 207
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 182 MTNHSFCLIKYGHILRVNQTENMTTK 209
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 208 ITSNSFVCLIKYGHILRVNQTENMTTK 235
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

## RESULT 14

```

ID 09NOTO PRELIMINARY; PRT; 235 AA.
AC 09NOTO;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE T-CELL CO-STIMULATORY PROTEIN B7-1.
GN B7-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Knutson T., Ma Z., Onishi T.;
RT "Cloning and Sequencing of canine CDNA encoding T-cell co stimulatory
RT molecule B7-1.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257653; AAF69006.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_1.
DR SMART; SM00410; IG_Like; 1.
SO SEQUENCE 235 AA; 26933 MW; C0EA51DA9FB224E3 CRC64;

```

Query Match 61.4%; Score 705; DB 6; Length 235;  
 Best Local Similarity 61.5%; Pred. No. 9,7e-58;  
 Matches 128; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

```

QY 2 LSHFCGVIHYTKVEKVALSCGHNVSEBELAOTRIYQEKKMYLTMMGDMNIMPEY 61
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 28 LEFYFCGIIQVKNKYKVEKVALSCDYNSTTELMKRYIWKQKDEVLAVYSGOTKWSKY 87
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 62 KNRITFDITNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFPPTSI 121
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 88 ENRTFADFTNNLSVILLALRPSDEGTECYVLAKE-KDAKREHLAEVTLVSKADFPPTSI 147
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 122 SDFEITPSNIRRICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSKLDEN 181
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 148 TDLGNPSPIRRLICTSGGFPPEPHLSWLENGEELNAINTVVSQDETELYAVSSKLDEN 207
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 182 MTNHSFCLIKYGHILRVNQTENMTTK 209
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 208 ITSNSFVCLIKYGHILRVNQTENMTTK 235
  | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

## RESULT 15

```

ID 035187 PRELIMINARY; PRT; 321 AA.
AC 035187;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE B7.1.
GN B7.1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FISCHER.
RA MEDLINE=99176648; PubMed=10078962;
RA Visse E., Slesjö P., Widegren B., Sjogren H.O.;
RT "Regression of intracerebral rat glioma isografts by therapeutic
RT subcutaneous immunization with interferon-gamma, interleukin-7, or
RT B7-1-transfected tumor cells.";
RL Cancer Gene Ther. 6:37-44(1999).

```

DR EMBL: AF010465; AAB66351.1; -  
DR InterPro: IPR003599; Ig\_  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; Ig; 1.  
DR SMART: SM00410; Ig\_Like; 1.  
SQ SEQUENCE 321 AA; 36351 MW; 071C6007FBBD1E60 CRC64;

Query Match 52.5%; Score 603.5; DB 11; Length 321;  
Best Local Similarity 54.9%; Pred. No. 4.1e-48;  
Matches 113; Conservative 34; Mismatches 58; Indels 1; Gaps 1;

OY 1 GLSHFGSVI-HYTKKKEVATLSCGHNVSEELAQRIYWKQKKVYLTMSGDNIWP 59  
DB 31 GLPQISSGIVGQVSKSVREKALLSCDKECSEOSIHRITYWKHKVYLSVISGVPEWVP 90  
OY 60 EYKNRTIFDITNNLSIVIALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPT 119  
DB 91 EYKNRTVYDIANNYSFSLGLILSDRGTYTCVQRYEGESYVVKHLITVELSVRADFPPT 150  
OY 120 STSDEIPIPTSNIRIICSTSGGFPEPHLSWLENGEELNAINITVSODPETELVAVSSKLD 179  
DB 151 NITESGNPSPADIRITCFASGGFPKPRLSWLENGRELINGINTTISQDPESSELYTISQLD 210  
OY 180 FNMETNHSFMCCLKYGHLYRNQTFENW 205  
DB 211 FNTTYDHFIDCFLEYGDHAYSONFTW 236

Search completed: October 17, 2002, 16:37:54  
Job time : 29 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Comphen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 16:35:35 ; Search time 31 Seconds  
(without alignments)  
773.934 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149  
Sequence: 1 GLSHFCSGVHYTKVEKVA.....LRVNOTFNMTKQEHDPN 216

Scoring table: BLOCUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	16	AA67989 Human B lymphocyte
2	1149	100.0	288	18	AAW38414 B7-1. Homo sapien
3	1149	100.0	288	20	AAW67804 Human B7 protein s
4	1149	100.0	288	20	AAW73640 Human B7-2 antigen
5	1149	100.0	288	21	AAW37087 Human B lymphocyte
6	1149	100.0	288	21	AAW99666 Human B7 protein.
7	1149	100.0	288	21	AAW44288 Human B7.1 co-stim
8	1149	100.0	288	21	AAW54920 Human B7.1 protein
9	1149	100.0	288	22	AAW05121 Colorectal tumour
10	1149	100.0	288	22	AAW19959 Human B lymphocyte
11	1149	100.0	473	18	AAW41415 Human B7.1-murine

12	1146	99.7	251	20	AAW90208
13	1144	99.6	475	18	AAW38415
14	1143	99.5	488	20	AAW86004
15	1143	99.5	488	22	AAW83836
16	1143	99.5	492	19	AAW42338
17	1138	99.0	480	20	AAW90206
18	1047	91.1	208	18	AAW35858
19	761	66.2	229	22	AAW97780
20	743	64.7	232	21	AAW32283
21	743	64.7	292	21	AAW32276
22	739	64.3	292	21	AAW32284
23	739	64.3	292	21	AAW32277
24	719	62.6	304	20	AAW41075
25	705	61.4	235	20	AAW41077
26	561	48.8	306	16	AAW82893
27	561	48.8	306	16	AAW67990
28	561	48.8	306	22	AAW19960
29	561	48.8	320	16	AAW82892
30	558	48.6	306	20	AAW67805
31	558	48.6	306	20	AAW73641
32	558	48.6	306	21	AAW37088
33	558	48.6	306	21	AAW9967
34	349.5	30.4	173	20	AAW41082
35	311	27.1	214	16	AAW82901
36	305	26.5	200	16	AAW82900
37	250.5	21.8	212	16	AAW82902
38	250.5	21.8	226	16	AAW82903
39	200.5	17.4	329	21	AAW32285
40	200.5	17.4	329	21	AAW32278
41	200.5	17.4	332	20	AAW41079
42	188.5	16.4	280	20	AAW41078
43	182	15.8	244	20	AAW90209
44	182	15.8	246	20	AAW6005
45	182	15.8	246	22	AAW83837

## ALIGNMENTS

RESULT 1	AAW67989	standard; Protein: 288 AA.
XX	AAW67989;	
AC	21-AUG-1995	(first entry)
XX	Human B lymphocyte antigen B7-1 (hb7-1).	
XX	B lymphocyte antigen; B7-1; B cell activation antigen; CD28;	
KW	ligand; T cell surface antigen; transmembrane protein.	
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FX	Protein	1..34
FT		/label= "signal sequence"
FT	Domain	35..242
FT		/label= extracellular
FT	Domain	243..269
FT		/label= transmembrane
FT	Domain	270..288
FT		/label= intracellular
FT	Misc-difference	53..55
FT		/label= N-linked glycosylation
FT	Misc-difference	89..91
FT		/label= see above
FT	Misc-difference	98..100
FT		/label= see above
FT	Misc-difference	186..188
FT		/label= see above
FT	Misc-difference	207..209

hb7.1glu-glu solub  
Soluble B7-1-19.  
Human B7-1.574.1 p  
Amino acid sequenc  
CD80-1g-alpha-tf f  
hb7.1fc soluble fu  
Human B7.1 for use  
Soluble porcine B7  
Feline CD80 (B7-1)  
Cat CD80 (B7-1)-TA  
Feline CD80 (B7-1)  
Cat CD80 (B7-1)-SY  
Canine B7-1 protei  
Canine B7-1S prote  
Mouse B7-1 alterna  
Murine B lymphocyt  
Mouse B lymphocyte  
Mouse B7-1 alterna  
Mouse B7 protein s  
Mouse B7-2 antigen  
Murine B lymphocyt  
Murine B7 protein.  
Feline B7-1S prote  
Mouse B7-1 (IGV-11  
Mouse B7-1 (IGV-11  
Mouse B7-1 (IGV-11  
Mouse B7-1 IgV-11k  
Feline CD86 (B7-2)  
Cat CD86 (B7-2) 11  
Feline B7-2S prote  
Canine B7-2S prote  
hb7.1his soluble f  
Human B7-2 extrac  
Amino acid sequenc

FT Misc-difference 211..213 /label= see above  
 FT Misc-difference 226..228 /label= see above  
 FT Misc-difference 232..234 /label= see above  
 FT Domain 35..138 /label= Ig V-set domain  
 FT Domain 139..236 /label= Ig C-set domain  
 FT W09503408-A.  
 XX  
 PD 02-FEB-1995.  
 XX  
 PF 26-JUL-1994; 94WO-0508423.  
 XX  
 PR 26-JUL-1993; 93US-0101624.  
 PR 19-AUG-1993; 93US-0109393.  
 PR 03-NOV-1993; 93US-0147773.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPR ) REPLIGEN CORP.  
 XX  
 PI Freeman GJ, Gray GS, Greenfield E, Nadler LM;  
 XX  
 DR WPI: 1995-075236/10.  
 DR N-PSDB: AAO81371.  
 XX  
 PT Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful  
 PT for enhancing or suppressing T-cell mediated immune responses  
 XX  
 PS Disclosure: pages 111-113; 175pp; English.  
 XX  
 CC Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,  
 CC cell line Raji, clone no. 13. Its position in the genome is  
 CC chromosome/segment 3. It was published by Freeman, P.J. et al.,  
 CC J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be  
 CC found in Genbank at Accession no. M27533. The encoded protein,  
 CC B67989, binds both human CTLA4 and human CD28. It is related  
 CC to human hb7-2 (see Q81351) and murine hb7 (see Q81372).  
 CC  
 XX  
 SQ Sequence 288 AA;  
 Query Match 100.0%; Score 1149; DB 16; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GISHFCGVIHVTKEVATLSCGHNVSEELAQTRITYOKKKVLTMMSGDMNIMPE 60  
 Db 27 GISHFCGVIHVTKEVATLSCGHNVSEELAQTRITYOKKKVLTMMSGDMNIMPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTVECVLYKEDAFKREHLAEVTLVSKADPTPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDEGTVECVLYKEDAFKREHLAEVTLVSKADPTPS 146  
 QY 121 ISDFEIPISNIRRICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180  
 Db 147 ISDFEIPISNIRRICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 206  
 QY 181 NMTNHSFMCCLKYGHILRVNQTFFNMNTTKQEHFPDN 216  
 Db 207 NMTNHSFMCCLKYGHILRVNQTFFNMNTTKQEHFPDN 242  
 RESULT 2  
 AAM38414  
 ID AAM38414 standard; Protein; 288 AA.  
 XX  
 AC AAM38414;  
 XX  
 OS 08-APR-1998 (first entry)  
 FT

XX  
 DE B7-1.  
 XX  
 KW Screening; inhibitor; enhancer; binding; CD28; B7-1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP795554-A2.  
 XX  
 PD 17-SEP-1997.  
 XX  
 PF 04-MAR-1997; 97EP-0301438.  
 XX  
 PR 02-OCT-1996; 96JP-0262085.  
 PR 05-MAR-1996; 96JP-0047795.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Hattori M, Hida T, Kurokawa T, Nakanishi A;  
 XX  
 DR WPI: 1997-450803/42.  
 DR N-PSDB: AAT96358.  
 XX  
 PT New xanthene derivatives useful as immunomodulators - e.g. methyl  
 PT 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-methyl  
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.  
 XX  
 PS Disclosure: Fig 4; 117pp; English.  
 XX  
 CC The present sequence was used in the development of a novel method  
 CC for screening for compounds that inhibit or enhance binding of CD28  
 CC to B7-1.  
 XX  
 SQ Sequence 288 AA;  
 Query Match 100.0%; Score 1149; DB 18; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GISHFCGVIHVTKEVATLSCGHNVSEELAQTRITYOKKKVLTMMSGDMNIMPE 60  
 Db 27 GISHFCGVIHVTKEVATLSCGHNVSEELAQTRITYOKKKVLTMMSGDMNIMPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTVECVLYKEDAFKREHLAEVTLVSKADPTPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDEGTVECVLYKEDAFKREHLAEVTLVSKADPTPS 146  
 QY 121 ISDFEIPISNIRRICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 180  
 Db 147 ISDFEIPISNIRRICSTSGGPEPHLSWLENGEELNAINITVSQDPETELAVSSKIDF 206  
 QY 181 NMTNHSFMCCLKYGHILRVNQTFFNMNTTKQEHFPDN 216  
 Db 207 NMTNHSFMCCLKYGHILRVNQTFFNMNTTKQEHFPDN 242  
 RESULT 3  
 AAM67804  
 ID AAM67804 standard; Protein; 288 AA.  
 XX  
 AC AAM67804;  
 XX  
 DE 13-APR-1999 (first entry)  
 XX  
 DE Human B7 protein sequence.  
 XX  
 KW Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;  
 KW T-cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..34

QY	1	27
Query Match	100.0%	Score 1149; DB 20; Length 288;
Best Local Similarity	100.0%;	Pred. No. 2,6e-103;
Matches 216; Conservative	0; Mismatches 0; Indels 0;	Gaps 0;
1	GSHPGSGYIHATKEKVAATLSCGHNVSVEELAQRIRYWKREKKVLTMMSGDNIMPE	60
27	GSHPGSGYIHATKEKVAATLSCGHNVSVEELAQRIRYWKREKKVLTMMSGDNIMPE	86

OY	61	YKNRTIEDITNNLSIVIALRPSDEGTCEVLAKEKDAFKREHLAEVTLSSKADFPPTS	120
Dd	87	YKNRTIEDITNNLSIVIALRPSDEGTCEVLAKEKDAFKREHLAEVTLSSKADFPPTS	146
OY	121	ISDFEIPTSNRIIRICSTSGGFPPEPHLSWLENGEDLNAINTVSODPETELIYAASSKLDF	180
Dd	147	ISDFEIPTSNRIIRICSTSGGFPPEPHLSWLENGEDLNAINTVSODPETELIYAASSKLDF	206
OY	181	NMTNHSPFCLIKYGHLRVNOTFNKNTTKOEHFPDN	216
Dd	207	NMTNHSPFCLIKYGHLRVNOTFNKNTTKOEHFPDN	242
 RESULT 4 AAW73640 ID AAW73640 standard; Protein; 288 AA.			
AC	XX	AAW73640;	
AC	XX	23-MAR-1999 (first entry)	
DX	DE	Human B7-2 antigen.	
XX	XX	B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;	
KW	XX	CTLA4 ligand; therapy; T-cell response; human.	
XX	XX	Homo sapiens.	
PN	XX	US5861310-A.	
PD	XX	19-JAN-1999.	
PF	XX	30-MAY-1995; 95US-0456104.	
PR	XX	30-MAY-1995; 95US-0456104.	
PR	XX	03-NOV-1993; 93US-0147773.	
PA	XX	(DAND ) DANA FARMER CANCER INST INC.	
PI	XX	Freeman GJ, Gray GS, Nadler LM;	
DR	XX	WPI, 1999-130394/11.	
DR	XX	N-P5DB; AAV55786.	
PT	XX	Tumour cell transfected to express B7-2 molecule - useful for tumour	
PT	XX	therapy by stimulating T-cell response	
PS	XX	Disclosure; Column 37-40; 27pp; English.	
CC	XX	This sequence is the human B7-2 antigen, which can be used in the	
CC	XX	method of the invention. The method is for transfecting an isolated	
CC	XX	mammalian tumour cell with an exogenous nucleic acid molecule encoding a	
CC	XX	mammalian B7-2 molecule, where the B7-2 molecule is expressed in the	
CC	XX	tumour cell is capable of costimulating a T cell and is capable of	
CC	XX	binding a CD28 or CTLA4 ligand. The method is useful for treating tumours	
CC	XX	by stimulating a T-cell response against tumour cells in vivo.	
SO	Sequence	288 AA:	
 Query Match 100.0%; Score 1149; DB 20; Length 288; Best Local Similarity 100.0%; Pred. No. 2,6e+103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
OY	1	GSHFCSGVIHTKYKVEKAATLSCGHNVSEELAQTRIYMOKEKKVLTMMSGDMNIWPE	60
Dd	27	GSHFCSSGIHTKYKVEKAATLSCGHNVSEELAQTRIYMOKEKKVLTMMSGDMNIWPE	86
OY	61	YKNRTIEDITNNLSIVIALRPSDEGTCEVLAKEKDAFKREHLAEVTLSSKADFPPTS	120
Dd	87	YKNRTIEDITNNLSIVIALRPSDEGTCEVLAKEKDAFKREHLAEVTLSSKADFPPTS	146
OY	121	ISDFEIPTSNRIIRICSTSGGFPPEPHLSWLENGEDLNAINTVSODPETELIYAASSKLDF	180
Dd	147	ISDFEIPTSNRIIRICSTSGGFPPEPHLSWLENGEDLNAINTVSODPETELIYAASSKLDF	206
OY	181	NMTNHSPFCLIKYGHLRVNOTFNKNTTKOEHFPDN	216
Dd	207	NMTNHSPFCLIKYGHLRVNOTFNKNTTKOEHFPDN	242

DB 147 ISDEIPTSNIRRIICSTSGGFPPEPHLSWLNCEELNAINTVTSODEPETELVAVSSKIDF 206  
 QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216  
 DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 5  
 AAB37087  
 ID AAB37087 standard; Protein: 288 AA.  
 AC AAB37087;  
 DT 28-MAR-2001 (first entry)  
 DE Human B lymphocyte antigen B7-1.  
 XX  
 XX Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;  
 KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;  
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;  
 KW T cell-mediated immune response; transplantation; vaccination.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6130316-A.  
 XX  
 PD 10-OCT-2000.  
 XX  
 PE 26-JUL-1994; 94US-0280757.  
 XX  
 PR 26-JUL-1993; 93US-0101624.  
 PR 19-AUG-1993; 93US-0109393.  
 PR 03-NOV-1993; 93US-0147773.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPK ) REPLIGEN CORP.  
 XX  
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;  
 DR MPI: 2000-655681/63.  
 DR N-PSDB: AAC84051.  
 XX  
 PT Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for  
 PT enhancing or suppressing T cell-mediated immune responses, especially  
 PT during tissue, skin or organ transplantation, or in graft-versus-host  
 PT disease -  
 XX  
 PS Disclosure: Column 87-90; 83pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule encoding a  
 CC fusion protein comprising a first nucleotide sequence encoding a first  
 CC peptide, and a second nucleotide sequence encoding a second peptide.  
 CC The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium  
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C  
 CC to a portion of a nucleotide sequence which encodes a human or murine  
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has  
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid  
 CC sequence that is identical or at least 50% identical with the  
 CC extracellular domain of a human B7-2 peptide (AAB37085). The second  
 CC peptide is especially an immunoglobulin constant region. This sequence  
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for  
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example  
 CC of a first peptide sequence of the invention. The nucleic acid molecules  
 CC are useful in various expression vectors to direct synthesis of the  
 CC corresponding proteins or peptides in a variety of hosts, particularly  
 CC eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic  
 CC acids are also useful for enhancing the immunogenicity of a mammalian  
 CC cell, e.g. tumour cell (sarcoma) or an antigen presenting cell  
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or  
 CC suppressing T cell-mediated immune responses, e.g. in situations of  
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.  
 CC The proteins are also useful for enhancing the efficacy of vaccination

CC against a variety of pathogens, and may also be used to upregulate an  
 CC immune response against a particular pathogen during an infection or  
 CC against a tumour in a tumour-bearing host.  
 XX  
 SQ Sequence 288 AA:  
 Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2,6e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GUSHPCSGVIHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIMPE 60  
 DB 27 GLSHPCSGVIHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIMPE 86  
 QY 61 YKNRTTFDITNNLSIYIILALRPSDEGTGECVYLYKEDAKRREHLAVTISVADFPPTPS 120  
 DB 87 YKNRTTFDITNNLSIYIILALRPSDEGTGECVYLYKEDAKRREHLAVTISVADFPPTPS 146  
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLNCEELNAINTVTSODEPETELVAVSSKIDF 180  
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLNCEELNAINTVTSODEPETELVAVSSKIDF 206  
 QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216  
 DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 6  
 AAY99966  
 ID AAY99966 standard; Protein: 288 AA.  
 AC AAY99966;  
 DT 10-JAN-2001 (first entry)  
 DE Human B7 protein.  
 XX  
 KW B7; human; B cell activation antigen; B lymphocytes;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;  
 KW herpes simplex; influenza; common cold; HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key  
 FT Peptide  
 FT Domain  
 FT Domain  
 FT Domain  
 FT Modified-site  
 FT Modified-site  
 FT Modified-site  
 FT Modified-site  
 FT Domain  
 FT Modified-site  
 FT Modified-site  
 FT Modified-site  
 FT Modified-site  
 FT Domain  
 FT Domain  
 FT Domain  
 FT Domain

Location/Qualifiers  
 1..34  
 /label= signal\_peptide  
 35..242  
 /label= extracellular\_domain  
 35..138  
 /label= "Ig V-set domain"  
 53..55  
 /note= "N-linked glycosylation site"  
 89..91  
 /note= "N-linked glycosylation site"  
 98..100  
 /note= "N-linked glycosylation site"  
 139..236  
 /label= "Ig C-set domain"  
 186..188  
 /note= "N-linked glycosylation site"  
 207..209  
 /note= "N-linked glycosylation site"  
 211..213  
 /note= "N-linked glycosylation site"  
 226..228  
 /note= "N-linked glycosylation site"  
 232..234  
 /note= "N-linked glycosylation site"  
 243..269  
 /label= Transmembrane\_domain  
 270..288  
 /label= Intracellular\_domain



PN US6071716-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 15-NOV-1993; 93US-0153262.  
 XX  
 PR 28-AUG-1991; 91US-0751306.  
 PR 01-OCT-1990; 90US-0591300.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PI Nadler LM, Freeman GJ, Freedman AS;  
 DR N-PSDB; AAA61328.  
 XX  
 PF 2000-422081/36.  
 DR  
 XX  
 PT New polynucleotides encoding a B7 activation antigen, useful for  
 PT regulating T cell mediated immune responses or viral diseases -  
 XX  
 PS Claim 1; Fig 4; 36pp; English.

CC The present sequence is the unique human B cell activation antigen B7  
 CC protein. The cDNA encoding this sequence was isolated from a Burkitt  
 CC lymphoma cell line cDNA library. Selection of cDNA clones was based  
 CC on expression of B7, as detected by the anti-B7 monoclonal antibody.  
 CC The human B7 cDNA was used in hybridisation analysis to isolate the  
 CC murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be  
 CC used to generate transgenic, knock-out animals which, in turn, are  
 CC useful in the development and screening of therapeutically useful  
 CC reagents. The expressed B7 protein is useful for enhancing or  
 CC blocking activated T cell mediated immune responses and immune  
 CC function. Modification of B7 expression is useful in the treatment of  
 CC autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),  
 CC herpes simplex, influenza, the common cold and HIV. It is also useful  
 CC in tissue and organ transplantation.

CC  
 XX  
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEKVEVATLSCGHNVSEELAQTRITWQEKEMVLTMMSGDNIMPE 60  
 DB 27 GLSHFCGVIHVTKEKVEVATLSCGHNVSEELAQTRITWQEKEMVLTMMSGDNIMPE 86  
 QY 61 YKNRTIEDITNNLSIVIALRPSDEGTVECVVLYEKDAFKREHLAEVTLGVKADFPPTS 120  
 DB 87 YKNRTIEDITNNLSIVIALRPSDEGTVECVVLYEKDAFKREHLAEVTLGVKADFPPTS 146  
 QY 121 ISDEFIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELVAVSSKIDF 180  
 DB 147 ISDEFIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELVAVSSKIDF 206  
 QY 181 NMTTNHSPMCLIKYGHLEVRNQTFFNMNTTKQEHFPDN 216  
 DB 207 NMTTNHSPMCLIKYGHLEVRNQTFFNMNTTKQEHFPDN 242

RESULT 7  
 AAY44289  
 ID AAY44289 standard; Protein: 288 AA.  
 XX  
 AC AAY44289;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Human B7.1 co-stimulatory molecule.  
 XX  
 KW Human B7.1 co-stimulatory molecule; antigen presenting cell;  
 KW immune response; cell surface receptor; Major histocompatibility complex;  
 KW MHC classII; proton motor force; mitochondrial membrane potential;  
 KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;

KW neurodegenerative disorder.

OS Homo sapiens.

XX W09953953-A2.

XX 28-OCT-1999.

XX 30-MAR-1999; 99WO-US06874.

XX 17-APR-1998; 98US-0082250.

XX 29-JUL-1998; 98US-0094519.

XX 24-SEP-1998; 98US-0101580.

XX (UYVE-) UNIV VERMONT.

XX Newell MK;

XX WPI; 2000-096773/08.

XX N-PSDB; AA229320.

XX Use of cell surface and membrane characteristics for developing  
 XX products for treating cancers, autoimmune diseases or neurodegenerative  
 XX diseases -  
 XX  
 XX Disclosure; Page 115; 123pp; English.

CC The present sequence is human B7.1 co-stimulatory molecule. This is  
 CC a glycoprotein on the surface of antigen presenting cells. This is  
 CC involved in stimulation of an immune response by its ability to interact  
 CC with various immune cell surface receptors. The regulation of cell  
 CC surface expression of MHC classII and co-stimulatory molecule B7 can be  
 CC manipulated by regulating the intracellular dissipation of proton motor  
 CC force which can be assessed in terms of mitochondrial membrane potential.  
 CC These methods can be used for regulating cell growth and division to  
 CC control disease processes by manipulating mitochondrial metabolism and  
 CC the expression of cell surface immune proteins. They can be used for  
 CC treating diseases associated with excessive cellular division, aberrant  
 CC differentiation, and premature cellular death, e.g. cancers, autoimmune  
 CC diseases, neurodegenerative disorders etc.

CC  
 XX  
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEKVEVATLSCGHNVSEELAQTRITWQEKEMVLTMMSGDNIMPE 60  
 DB 27 GLSHFCGVIHVTKEKVEVATLSCGHNVSEELAQTRITWQEKEMVLTMMSGDNIMPE 86  
 QY 61 YKNRTIEDITNNLSIVIALRPSDEGTVECVVLYEKDAFKREHLAEVTLGVKADFPPTS 120  
 DB 87 YKNRTIEDITNNLSIVIALRPSDEGTVECVVLYEKDAFKREHLAEVTLGVKADFPPTS 146  
 QY 121 ISDEFIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELVAVSSKIDF 180  
 DB 147 ISDEFIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSODPETELVAVSSKIDF 206  
 QY 181 NMTTNHSPMCLIKYGHLEVRNQTFFNMNTTKQEHFPDN 216  
 DB 207 NMTTNHSPMCLIKYGHLEVRNQTFFNMNTTKQEHFPDN 242

RESULT 8  
 AAY54920  
 ID AAY54920 standard; Protein: 288 AA.  
 XX  
 AC AAY54920;  
 XX  
 DT 14-FEB-2000 (first entry)  
 XX  
 DE Human B7.1 protein sequence.

XX Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;  
KM IL-12 p40 subunit; gene therapy; tumour; Leukaemia; B7.1 protein.  
XX

OS Homo sapiens.  
XX

PN US5994104-A.  
XX

PD 30-NOV-1999.  
XX

PF 08-NOV-1996; 96US-0751767.  
XX

PR 08-NOV-1996; 96US-0751767.  
XX

PA (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
XX

PI Anderson RJ, Prentice HG, MacDonald ID;  
XX

DR WPI; 2000-038261/03.  
XX

DR N-PSDB; AA240022.  
XX

PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful  
XX for treating leukemia and other cancers .

PS Example; Fig 10; 73pp; English.  
XX

CC This sequence represents the human B7.1 protein sequence.  
CC

CC The invention relates to an isolated nucleic acid construct (I)  
CC comprising a region encoding an interleukin-12 (IL-12) fusion protein

CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker  
CC peptide (joining the subunits)) and a region encoding a B7 protein. (I)

CC may be used to produce IL-12 fusion proteins according to standard  
CC recombinant DNA methodologies. The fusion proteins may be produced either

CC in vitro in a fermentation culture or in vivo as part of a gene therapy  
CC protocol (in this case (I) is used to transform a patient's cells, which

CC then secrete the functional polypeptide to supplement the patients own  
CC production of IL-12 or to rectify mutations which lead to the expression

CC of inactive polypeptides). The fusion proteins produced in this way may  
CC be used to treat any disease which responds to IL-12 such as tumours

CC (both solid and dispersed of the kidney, breast, colon, ovarian and  
CC cervical tumours and melanomas) and in particular, tumours of the blood

CC such as leukaemia. Alternatively, the polypeptides may be used as  
CC antigens in the production of antibodies to IL-12 and to assay for

CC agonists and antagonists of its activity. The antibodies and antagonists  
CC may be used to inhibit the activity of IL-12. (I) may also be used

CC diagnostically as a probe which hybridizes to sequences encoding IL-12  
CC and the antibodies may be used to detect the presence of IL-12

CC polypeptides in samples. They may be used diagnostically to quantitate  
CC the expression of the polypeptide by patients and hence which subjects

CC may be in need of restorative therapy.  
XX

SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;  
Best Local Similarity 100.0%; Pred. No. 2.6e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSGVHYHTKEVKEVATLSCGHNVSEELATRIYMOKEKMYLTMNSGDMNIME 60  
DB 27 GLSHFGSGVHYHTKEVKEVATLSCGHNVSEELATRIYMOKEKMYLTMNSGDMNIME 86

QY 61 YKNRTIPDITNNLSIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPPTS 120  
DB 87 YKNRTIPDITNNLSIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPPTS 146

QY 121 ISDEIPITSNIRITICSGSGFPPEPHLSWLENGEELNAINITVSODPETELIYAVNSKIDF 180  
DB 147 ISDEIPITSNIRITICSGSGFPPEPHLSWLENGEELNAINITVSODPETELIYAVNSKIDF 206

QY 181 NMTNHSFMCILIKYGHLEFVNQTFNMNTTKQEHFPDN 216  
DB 207 NMTNHSFMCILIKYGHLEFVNQTFNMNTTKQEHFPDN 242

RESULT 9  
ID AAU05121 standard; Protein; 288 AA.  
XX AAU05121;  
AC AAU05121;  
XX

DT 24-OCT-2001 (first entry)  
XX

DE Colorectal tumour antigen CD80.  
XX

XX Colorectal cancer; immunostimulant; cytostatic; immune response;  
KW adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;  
KW SW403 cell; colon; breast; lung; prostate; cancer; vaccine;  
KW tumour antigen CD80.  
XX

XX Homo sapiens.  
OS

XX WO200154716-A2.  
PN

XX 02-AUG-2001.  
PD

XX 26-JAN-2001; 2001WO-US02731.  
PF

XX 27-JAN-2000; 2000US-0178498.  
PR

XX 28-FEB-2000; 2000US-0185335.  
XX

XX (KIMM-) KIMMEL CANCER CENT. SYDNEY.  
PA

XX (JMM-) IMMUNE RESPONSE CORP.  
XX

XX Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;  
PI

XX WPI; 2001-502616/55.  
DR

XX N-PSDB; AA511426.  
DR

XX New composition comprising an allogeneic tumour cell, useful for  
PT stimulating an immune response in a patient having an adenocarcinoma,  
PT especially useful for treating colorectal, breast, lung or prostate  
PT cancer .

XX Example 2; Page 130-131; 131pp; English.  
XX

XX The invention relates to a composition for stimulating an immune response  
XX in a patient having an adenocarcinoma or colorectal cancer. The

XX composition comprises an allogeneic tumour cell selected from SW620 cell,  
XX COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic

XX cell stimulates an immune response to an autologous tumour cell in the  
XX patient. The composition is useful for stimulating an immune response in

XX a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate  
XX adenocarcinoma. The use of allogeneic tumour cells provides a generic

XX source of antigen that can be administered to a variety of patients, in  
XX contrast to using autologous tumour cells, which must be isolated from

XX each individual patient. The allogeneic cells are suitable as a cancer  
XX vaccine and can stimulate an immune response against autologous tumour

XX cells of a cancer patient. The present sequence represents the amino acid  
XX sequence of colorectal tumour antigen CD80 used in the method of the  
XX invention.  
XX

SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;  
Best Local Similarity 100.0%; Pred. No. 2.6e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSGVHYHTKEVKEVATLSCGHNVSEELATRIYMOKEKMYLTMNSGDMNIME 60  
DB 27 GLSHFGSGVHYHTKEVKEVATLSCGHNVSEELATRIYMOKEKMYLTMNSGDMNIME 86

QY 61 YKNRTIPDITNNLSIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPPTS 120  
DB 87 YKNRTIPDITNNLSIVIALRPSDEGTYECVLYKEKDAFKREHLAEVTLVSKADFPPTS 146

QY 121 ISDEIPITSNIRITICSGSGFPPEPHLSWLENGEELNAINITVSODPETELIYAVNSKIDF 180

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DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLNGBELNAINTTVSODPETELIYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 10
AAB19959
ID AAB19959 standard; Protein; 288 AA.
XX
AC AAB19959;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human B lymphocyte antigen B7.
XX
KW Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
KW CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
KW metastasis; antitumour; therapy.
XX
OS Homo sapiens.
XX
FH Key 1 Location/Qualifiers
FT Peptide 1..34 /label= Signal_peptide
FT Protein 35..288 /label= Mature_protein
FT Domain 35..242 /note= "extracellular domain"
FT Domain 243..269 /note= "transmembrane domain"
FT Domain 270..288 /note= "intracellular domain"
FT Domain 35..138 /note= "immunoglobulin V-set domain"
FT Domain 139..236 /note= "immunoglobulin C-set domain"
FT Modified-site 53..55 /note= "Asn is N-glycosylated"
FT Modified-site 89..91 /note= "Asn is N-glycosylated"
FT Modified-site 98..100 /note= "Asn is N-glycosylated"
FT Modified-site 186..188 /note= "Asn is N-glycosylated"
FT Modified-site 207..209 /note= "Asn is N-glycosylated"
FT Modified-site 211..213 /note= "Asn is N-glycosylated"
FT Modified-site 226..228 /note= "Asn is N-glycosylated"
FT Modified-site 232..234 /note= "Asn is N-glycosylated"
XX
PN US6149905-A.
XX
PD 21-NOV-2000.
XX
PF 23-SEP-1998; 98US-0159135.
XX
PR 03-NOV-1993; 93US-0147772.
XX
PA (GEMV ) GENETICS INST INC.
PA (DAND ) DANA FARMER CANCER INST INC.
PA (HARD ) HARVARD COLLEGE.
XX
PI Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
PI Nadler LM;
XX
DR WPI; 2001-079388/09.
DR N-PSDB; AAA89224.

```

```

XX
PT Modifying tumor cell for treating tumors, reducing metastatic spread.
PT Inhibiting recurrence of tumor and increasing immunogenicity, involves
PT transfecting tumor cells with a nucleic acid encoding B7 molecule
PS Claim 4; Column 31-34; 24pp; English.
XX
CC The present sequence is that of human lymphocyte antigen B7, a T
CC cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
CC cells modified to express a T cell costimulatory molecule,
CC especially B7, are disclosed. The tumour cells are modified by
CC transfection with a nucleic acid encoding the T cell costimulatory
CC molecule, by using an agent which induces or increases expression
CC of the T cell costimulatory molecule on the tumour cell surface, or
CC by coupling the T cell costimulatory molecule to the tumour cell
CC surface. Tumour cells further modified to express major
CC histocompatibility complex (MHC) class I and/or class II molecules,
CC or in which expression of an MHC associated protein, the invariant
CC chain, is inhibited are also disclosed. The modified tumour cells
CC are used to treat a patient with a tumour, preventing or inhibiting
CC metastatic spread or tumour recurrence. The tumour may be a
CC melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
CC specifically inducing a CD4+ T cell response against a tumour, and a
CC method for treating a tumour by modification of tumour cells in vivo
CC are also disclosed. The treatment methods increase the immunogenicity
CC of the tumour cell in vivo. The antitumour T cell-mediated immune
CC response is effective both against the modified tumour cells and the
CC unmodified tumour cells from which the modified cells were derived.
CC Thus, the effector phase of the antitumour response induced by the
CC modified tumour cells is not dependent upon expression of a
CC costimulatory molecule on the tumour cells.
XX
SQ Sequence 288 AA;
Query Match 100.0%; Score 1149; DB 22; Length 288;
Best Local Similarity 100.0%; Pred. No. 2,6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHPCSGVHVTEKVEKAVATLSCGHNVSEELAQTRITPMQEKEMVLTMMSGDMNIMPE 60
DB 27 GLSHPCSGVHVTEKVEKAVATLSCGHNVSEELAQTRITPMQEKEMVLTMMSGDMNIMPE 86
QY 61 YKNRTIPDITNNLSIVILALRPSDEGYECVLYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIPDITNNLSIVILALRPSDEGYECVLYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLNGBELNAINTTVSODPETELIYAVSSKIDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLNGBELNAINTTVSODPETELIYAVSSKIDF 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKOEHPDN 242

RESULT 11
AAM41415
ID AAM41415 standard; Protein; 473 AA.
XX
AC AAM41415;
XX
DT 02-JUN-1998 (first entry)
XX
DE Human B7.1-murine A5B7 F(ab')2 fusion protein.
XX
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region.
XX
OS Chimeric - Homo sapiens.
XX
OS Chimeric - Mus sp.
XX
PN WO9742329-A1.

```

PD 13-NOV-1997.  
 XX  
 PF 29-APR-1997; 97WO-GB01165.  
 XX  
 PR 14-FEB-1997; 97GB-0003103.  
 PR 04-MAY-1996; 96GB-0009405.  
 PA (ZENE ) ZENECA LTD.  
 XX  
 XX Copley CG, Edge MD, Emery SC;  
 PI WPI: 1997-558987/51.  
 DR N-PSDB; AAV17340.  
 XX  
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for  
 PT diagnosis and therapy of cancer  
 XX  
 PS Reference Example 3; Page 190-193; 208pp; English.  
 XX  
 CC This sequence is the human B7.1-murine A5B7 F(ab')<sub>2</sub> fusion protein  
 CC (AB7), and is an example of the antibody of the invention. The antibody  
 CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably  
 CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA  
 CC encoding the antibody, are used to make the antibody or conjugate. The  
 CC conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The antibody can be used for in vivo or in vitro  
 CC diagnosis of cancer.  
 XX  
 SQ Sequence 473 AA;  
 Query Match 100.0%; Score 1149; DB 18; Length 473;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLSHFCSGVIHVTKEKEVATLSGHNVSVEELAQTRIRYQKEKKVLTMMSGDMNIWPE 60  
 DB 27 GLSHFCSGVIHVTKEKEVATLSGHNVSVEELAQTRIRYQKEKKVLTMMSGDMNIWPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTYECVLYKEDAFKREHLAEVTLISKADPTPS 120  
 DB 87 YKNRTIFDITNNLSIVIALRPSDEGTYECVLYKEDAFKREHLAEVTLISKADPTPS 146  
 QY 121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTVSODPETELAVAVSSKIDF 180  
 DB 147 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTVSODPETELAVAVSSKIDF 206  
 QY 181 NMTTNHSMCLIKYGHRLRVNQTFFNMNTTKQEHFPDN 216  
 DB 207 NMTTNHSMCLIKYGHRLRVNQTFFNMNTTKQEHFPDN 242  
 RESULT 12  
 AAW90208 standard; Protein; 251 AA.  
 ID AAW90208;  
 AC AAW90208;  
 XX  
 XX 10-MAY-1999 (first entry)  
 DE hb7.1glu-glu soluble fusion protein.  
 XX  
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;  
 KW CD86; T cell activation; inhibitor; graft versus host disease;  
 KW transplant rejection; allograft rejection; autoimmune disease;  
 KW allergy; therapy; human; hb7.1glu-glu.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - synthetic.  
 XX  
 XX Kgy Location/Qualifiers  
 FT Peptide 1..34  
 FT /note= "potential eukaryotic secretory signal

FT Domain 35..242 peptide"  
 FT /note= "human B7.1 (mature protein) extracellular  
 FT domain"  
 FT Peptide 243..251  
 FT /note= "Glu-Glu detection/purification tag"  
 PN W09858965-A2.  
 XX  
 XX 30-DEC-1998.  
 PD  
 PD 22-JUN-1998; 98WO-EP03791.  
 PF  
 PR 20-JUN-1997; 97EP-0870092.  
 PR (INNO-) INNOGENETICS NV.  
 PA Bosman A, Buyse M, Lorre K, Sablon E;  
 PI WPI: 1999-105615/09.  
 DR  
 XX  
 XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection  
 PS Example 3.1.2; Fig 4; 182pp; English.  
 XX  
 CC This 29 kDa soluble fusion protein, termed hb7.1glu-glu, is composed  
 CC of human co-stimulatory molecule B7.1 extracellular domain fused  
 CC C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It  
 CC was produced from total RNA of Epstein-Barr virus-transformed  
 CC human spleen cells by RT-PCR using primers MR67 and MR145 (see  
 CC AAX01601). The fusion protein has been produced in Sf9 Spodoptera  
 CC frugiperda insect cells using a baculovirus expression system.  
 CC The invention relates to molecules such as diabodies, trivalent and  
 CC tetravalent antibodies and small antigen binding peptides which can  
 CC cross-link, or cross-react with, B7.1 and B7.2 expressed on  
 CC professional antigen presenting cells leading to the inhibition of  
 CC antigen-specific T cell activation. Methods to produce such  
 CC molecules are provided. The molecules are used to treat or prevent  
 CC diseases of the immune system, in particular graft rejection, graft  
 CC versus host disease, allergy and autoimmune diseases (claimed).  
 XX  
 SQ Sequence 251 AA;  
 Query Match 99.7%; Score 1146; DB 20; Length 251;  
 Best Local Similarity 99.5%; Pred. No. 4.2e-103;  
 Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLSHFCSGVIHVTKEKEVATLSGHNVSVEELAQTRIRYQKEKKVLTMMSGDMNIWPE 60  
 DB 27 GLSHFCSGVIHVTKEKEVATLSGHNVSVEELAQTRIRYQKEKKVLTMMSGDMNIWPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTYECVLYKEDAFKREHLAEVTLISKADPTPS 120  
 DB 87 YKNRTIFDITNNLSIVIALRPSDEGTYECVLYKEDAFKREHLAEVTLISKADPTPS 146  
 QY 121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTVSODPETELAVAVSSKIDF 180  
 DB 147 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTVSODPETELAVAVSSKIDF 206  
 QY 181 NMTTNHSMCLIKYGHRLRVNQTFFNMNTTKQEHFPDN 216  
 DB 207 NMTTNHSMCLIKYGHRLRVNQTFFNMNTTKQEHFPDN 242  
 RESULT 13  
 AAW38415 standard; Protein; 475 AA.  
 ID AAW38415;  
 AC AAW38415;  
 XX  
 XX 08-APR-1998 (first entry)  
 DE

DE Soluble B7-1-Ig.  
 XX Screening; inhibitor; enhancer; binding; CD28; B7-1;  
 KW soluble B7-1-Ig; immunoglobulin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP795554-A2.  
 XX  
 PD 17-SEP-1997.  
 XX  
 PE 04-MAR-1997; 97EP-0301438.  
 XX  
 PR 02-OCT-1996; 96GP-0262085.  
 PR 05-MAR-1996; 96GP-0047795.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Hatfori M, Hida T, Kurokawa T, Nakanishi A;  
 XX  
 DR WPI. 1997-450803/42.  
 DR N-PSDB; AAT96359.  
 XX  
 PT New xanthene derivatives useful as immunomodulators - e.g. methyl  
 PT 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-  
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.  
 XX  
 PS Disclosure: Fig 6 and 7; 117pp; English.  
 XX  
 CC The present sequence was used in the development of a novel method  
 CC for screening for compounds that inhibit or enhance binding of CD28  
 CC to B7-1.  
 CC  
 XX Sequence 475 AA:  
 SQ  
 Query Match 99.6%; Score 1144; DB 18; Length 475;  
 Best Local Similarity 99.5%; Pred. No. 1.6e-102;  
 Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GUSHCSGVYHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIPE 60  
 DB 27 GUSHCSGVYHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTECVYLYKEKDAFKREHLAEVTLVSKADFPPTS 120  
 DB 87 YKNRTIFDITNNLSIVIALRPSDEGTECVYLYKEKDAFKREHLAEVTLVSKADFPPTS 146  
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELAVASSKIDF 180  
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELAVASSKIDF 206  
 QY 181 NMTNHSFMCILIKYGHLLRVNQTFFNNNTTKQEHFPD 216  
 DB 207 NMTNHSFMCILIKYGHLLRVNQTFFNNNTTKQEHFPD 242

RESULT 14  
 AAB86004  
 ID AAB86004 standard; Protein: 488 AA.  
 XX  
 AC AAB86004;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Human B7-1.5T4.1 protein fusion, specific for human 5T4.  
 KW Tumour interacting protein; cancer; gene therapy; vector;  
 KW 5T4 antigen; monoclonal antibody; single chain antibody;  
 KW mouse; human; B7-1; co-stimulatory molecule.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - synthetic.

XX  
 PN WO9855607-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PE 04-JUN-1998; 98WO-GB01627.  
 XX  
 PR 04-JUL-1997; 97GB-0014230.  
 PR 04-JUN-1997; 97GB-0011579.  
 PR 20-JUN-1997; 97GB-0013150.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI Bebbington CR, Carroll MW, Ellard FW, Kingsman SM;  
 PI Myers KA;  
 XX  
 DR WPI. 1999-059910/05.  
 DR N-PSDB; AAY80292.  
 XX  
 PT New vector encoding a tumour interacting protein for treating cancer  
 PT - contains a desired nucleotide sequence and/or protein which  
 PT recognises tumours, and is used as a gene delivery system to treat  
 PT cancer  
 PS  
 XX Example 5; Fig 2; 82pp; English.  
 XX  
 CC This is the amino acid sequence of B7-1.5T4.1, a fusion protein  
 CC comprising the extracellular domain (amino acids 1-215) of human  
 CC co-stimulatory molecule B7-1 joined via a flexible peptide linker  
 CC to an scFv (see AAB86002) derived from murine 5T4 monoclonal  
 CC antibody. B7-1.5T4.1 cDNA (see AAY80292) can be inserted into vector  
 CC PCI to allow expression of the fusion protein in mammalian cells.  
 CC The tropoblast cell surface antigen defined by 5T4 is expressed at  
 CC high levels on the cells of a wide variety of human tumours. The  
 CC invention relates to a vector comprising a nucleotide sequence  
 CC coding for a tumour interacting protein (TIP) and optionally a  
 CC nucleotide sequence of interest (NOI) which encodes a protein of  
 CC interest (POI), the vector being capable of delivering the NOI  
 CC and/or POI to the tumour recognised by the TIP. Delivery can be in  
 CC vivo or ex vivo. The vector is used to treat cancer, and may also  
 CC used as a gene delivery system for introducing at least 1 gene  
 CC encoding a TIP (preferably a tumour binding protein) into a  
 CC haematopoietic cell lineage. B7-1 is expected to bind specifically  
 CC to CD28 and CTLA-4 present on human T-cells.  
 CC  
 XX Sequence 488 AA:  
 SQ  
 Query Match 99.5%; Score 1143; DB 20; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GUSHCSGVYHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIPE 60  
 DB 27 GUSHCSGVYHVTKEKEVATLSCGHNVSEELAQTRIVYQKEKKVLTMMSGDMNIPE 86  
 QY 61 YKNRTIFDITNNLSIVIALRPSDEGTECVYLYKEKDAFKREHLAEVTLVSKADFPPTS 120  
 DB 87 YKNRTIFDITNNLSIVIALRPSDEGTECVYLYKEKDAFKREHLAEVTLVSKADFPPTS 146  
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELAVASSKIDF 180  
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELAVASSKIDF 206  
 QY 181 NMTNHSFMCILIKYGHLLRVNQTFFNNNTTKQEHFPD 215  
 DB 207 NMTNHSFMCILIKYGHLLRVNQTFFNNNTTKQEHFPD 241

RESULT 15  
 AAB83836  
 ID AAB83836 standard; Protein: 488 AA.  
 XX  
 AC AAB83836;

XX 23-JUL-2001 (first entry)  
 DT Amino acid sequence of a B7-1.5T4.1 fusion protein.  
 DE  
 XX  
 KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;  
 KW hypersensitivity; autoimmune disease; central nervous system disorder;  
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;  
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;  
 KW Helicobacter-related disease; immune disorder.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 XX WO200136486-A2.  
 PN  
 XX 25-MAY-2001.  
 PD  
 XX 13-NOV-2000; 2000WO-GB04317.  
 PF  
 XX 18-NOV-1999; 99WO-GB03859.  
 PR 15-FEB-2000; 2000GB-0003527.  
 PR 02-MAR-2000; 2000GB-0005071.  
 XX  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 PA  
 XX Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;  
 PI Myers KA;  
 PI  
 DR WPI: 2001-343805/36.  
 DR N-PSDB; AAF89730.  
 XX  
 XX Use of single chain antibody capable of recognizing a disease  
 PT associated molecule for manufacturing a medicament for preventing  
 PT and/or treating a disease condition associated with disease associated  
 PT molecule  
 PT  
 XX  
 XX Claim 3; Fig 2; 118pp; English.  
 PS  
 XX  
 CC The specification describes the use of a single chain antibody (ScFv),  
 CC which is capable of recognizing a disease associated molecule in the  
 CC manufacture of a medicament for the prevention and treatment of a  
 CC disease condition. The ScFv antibody is useful in the manufacture of  
 CC a medicament, for affecting a disease in vivo, for preparing a  
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant  
 CC treatment of a disease. The ScFv antibody is also useful for  
 CC treating inflammatory diseases including arthritis, hypersensitivity,  
 CC autoimmune diseases, cancers, central nervous system disorders  
 CC including Parkinson's disease, periodontal diseases, cardiopulmonary  
 CC diseases, cardiovascular diseases, gastrointestinal disorders,  
 CC infections, diabetes, Helicobacter-related diseases, and other immune  
 CC disorders. The present sequence represents a B7-1.5T4.1 fusion protein.  
 CC This comprises the N-terminus of the 5T4 ScFv is fused after amino acid  
 CC 215 of human B7-1.  
 CC  
 XX  
 XX Sequence 488 AA:  
 SQ

QY 181 NMTHSFMCLIKYGLRVNQTENNNTKOEHPD 215  
 DB 207 NMTHSFMCLIKYGLRVNQTENNNTKOEHPD 241

Search completed: October 17, 2002, 16:36:15  
 Job time : 33 secs

Query Match 99.5%; Score 1143; DB 22; Length 488;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-102;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHYTKVEKVAATLSCGHNVSVEELAQTRIVQKEKKVLTLMWSDMNIMPE 60  
 DB 27 GLSHFCGVIHYTKVEKVAATLSCGHNVSVEELAQTRIVQKEKKVLTLMWSDMNIMPE 86  
 QY 61 YKNRTFEDTTNNSTVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADFPPTS 120  
 DB 87 YKNRTFEDTTNNSTVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADFPPTS 146  
 QY 121 ISDFEIPITSNIRRIICSTSGGFEPEHLWLENGEELNAINTTVSQDPETELIYAVSSKIDF 180  
 DB 147 ISDFEIPITSNIRRIICSTSGGFEPEHLWLENGEELNAINTTVSQDPETELIYAVSSKIDF 206

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OM protein - protein search, using sw model

Run on: October 17, 2002, 16:35:40 ; Search time 13 Seconds  
(without alignments)  
405.841 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149  
Sequence: 1 GLSHFCGVHVTKEVEVA.....LRYNOTFNMTTKOEHFDPN 216

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCPUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	2 US-08-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2 US-08-456-104-6	Sequence 6, Appli
3	1149	100.0	288	2 US-08-101-624-23	Sequence 23, Appl
4	1149	100.0	288	2 US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3 US-08-153-262-2	Sequence 2, Appli
6	1149	100.0	288	3 US-08-479-744A-29	Sequence 29, Appl
7	1149	100.0	288	4 US-08-280-757B-29	Sequence 29, Appl
8	1149	100.0	288	4 US-09-159-135-2	Sequence 2, Appli
9	1149	100.0	288	4 US-08-205-697A-19	Sequence 19, Appl
10	1149	100.0	288	4 US-08-702-525-19	Sequence 19, Appl
11	1149	100.0	288	4 US-09-450-798-2	Sequence 2, Appli
12	1149	100.0	288	4 US-08-403-253A-2	Sequence 2, Appli
13	1149	100.0	288	5 PCT-US95-02576-19	Sequence 19, Appl
14	1149	100.0	473	4 US-09-171-945-131	Sequence 131, App
15	1102	95.9	208	4 US-09-460-384-36	Sequence 36, Appl
16	1050	91.4	208	3 US-08-630-172-15	Sequence 15, Appl
17	1050	91.4	208	4 US-09-375-419-15	Sequence 15, Appl
18	561	48.8	306	4 US-08-205-697A-17	Sequence 17, Appl
19	561	48.8	306	4 US-08-702-525-17	Sequence 17, Appl
20	561	48.8	306	5 PCT-US95-02576-17	Sequence 17, Appl
21	561	48.8	320	4 US-08-205-697A-2	Sequence 2, Appli
22	561	48.8	320	5 PCT-US95-02576-2	Sequence 2, Appli
23	561	48.8	306	2 US-08-147-772-4	Sequence 4, Appli
24	558	48.6	306	2 US-08-456-104-8	Sequence 8, Appli
25	558	48.6	306	2 US-08-101-624-25	Sequence 25, Appl
26	558	48.6	306	3 US-08-153-262-4	Sequence 4, Appli
27	558	48.6	306	3 US-08-153-262-4	Sequence 4, Appli

#### ALIGNMENTS

28	558	48.6	306	3 US-08-479-744A-31	Sequence 31, Appl
29	558	48.6	306	4 US-08-280-757B-31	Sequence 31, Appl
30	558	48.6	306	4 US-09-159-135-4	Sequence 4, Appli
31	558	48.6	306	4 US-09-450-798-4	Sequence 4, Appli
32	311	27.1	200	4 US-08-205-697A-9	Sequence 9, Appli
33	311	27.1	200	4 US-08-702-525-9	Sequence 9, Appli
34	311	27.1	200	5 PCT-US95-02576-9	Sequence 9, Appli
35	311	27.1	214	4 US-08-205-697A-11	Sequence 11, Appl
36	311	27.1	214	4 US-08-702-525-11	Sequence 11, Appl
37	311	27.1	214	5 PCT-US95-02576-11	Sequence 11, Appl
38	250.5	21.8	212	4 US-08-702-525-63	Sequence 63, Appl
39	250.5	21.8	212	5 PCT-US95-02576-63	Sequence 63, Appl
40	250.5	21.8	226	4 US-08-702-525-65	Sequence 65, Appl
41	250.5	21.8	226	5 PCT-US95-02576-65	Sequence 65, Appl
42	182	15.8	323	5 PCT-US94-09642-2	Sequence 2, Appli
43	182	15.8	329	2 US-08-456-104-2	Sequence 2, Appli
44	182	15.8	329	2 US-08-101-624-2	Sequence 2, Appli
45	182	15.8	329	3 US-08-479-744A-2	Sequence 2, Appli

RESULT 1  
US-08-147-772-2  
Sequence 2, Application US/08147772

Patent No. 5858776

GENERAL INFORMATION:

APPLICANT: Ostrand-Rosenberg, Suzanne

APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glumcher, Laurie H.

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,772

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

FEATURE: for CD8 T cell surface antigen; transmembrane protein

NAME/KEY: signal sequence

LOCATION: -34 to -1

IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-08-147-772-2  
Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSHPSGVYHWKKEKVAATLSCGHNVSYEEIAQFTIYQKEKKVLTWMSGDMNIWPE 60  
DB 27 GSHPSGVYHWKKEKVAATLSCGHNVSYEEIAQFTIYQKEKKVLTWMSGDMNIWPE 86  
QY 61 YNRTIEDITNNLSIVIALRPSDEGTVECVLAKYEDAKREHLAEVTLVSKADPTPS 120  
DB 87 YNRTIEDITNNLSIVIALRPSDEGTVECVLAKYEDAKREHLAEVTLVSKADPTPS 146  
QY 121 ISDFELPTSNIRITICSTSGGPEPHLSWLENGEELNAINFTVSODETELAVSSKLD 180  
DB 147 ISDFELPTSNIRITICSTSGGPEPHLSWLENGEELNAINFTVSODETELAVSSKLD 206  
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTQOEHPDN 216  
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTQOEHPDN 242  
RESULT 2  
US-08-456-104-6  
Sequence 6, Application US/08456104  
Patent No. 5861310  
GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,104  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/101,624;  
FILING DATE: 26-JUL-1993;  
APPLICATION NUMBER: 08/109,393;  
APPLICATION NUMBER: 19-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids



TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-456-104-6

Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5,2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFGSVHVRKEKVAATLSCGNVSVLEELAQRTYQKKEKMWLTMMSGDMNTWPE 60  
DB 27 GLSHFGSVHVRKEKVAATLSCGNVSVLEELAQRTYQKKEKMWLTMMSGDMNTWPE 86  
QY 61 YKRRITFDITNNLSIYIALRPSDEGTVECVLKYERDAFRREHLAEVTLVKNADPTPS 120  
DB 87 YKRRITFDITNNLSIYIALRPSDEGTVECVLKYERDAFRREHLAEVTLVKNADPTPS 146  
QY 121 ISDFEIPTSIRRIICSTSGGFPPEHLSWLENGEELNATITVSQDETELAVSSKLD 180  
DB 147 ISDFEIPTSIRRIICSTSGGFPPEHLSWLENGEELNATITVSQDETELAVSSKLD 206  
QY 181 NMTNHSFMCILIKYGHLRVQNTFNMTTKOEHPDN 216  
DB 207 NMTNHSFMCILIKYGHLRVQNTFNMTTKOEHPDN 242

## RESULT 3

US-08-101-624-23

Sequence 23, Application US/08101624

Patent No. 5942607

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands and

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE &amp; COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/101,624

FILING DATE: 26-JUL-1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

FEATURE: for CD28 T cell surface antigen; transmembrane protein

NAME/KEY: signal sequence

LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic

FEATURE: extracellular domain

NAME/KEY: 1 to 208

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: intracellular domain

LOCATION: 236 to 254

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 19 to 21

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 55 to 57

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 152 to 154

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 177 to 179

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig V-set domain

LOCATION: 1 to 104

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:

AUTHORS: FREEMAN, GORDON J.

AUTHORS: FREEDMAN, ARNOLD S.

AUTHORS: SEGIL, JEFFREY M.

AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262  
US-08-101-624-23

Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5.2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHFCSGVHYHTKEVEVATLSCGHNVSEELAQTRITYQKKEKKWLTMMSGDMNTWPE 60  
DB 27 GSHFCSGVHYHTKEVEVATLSCGHNVSEELAQTRITYQKKEKKWLTMMSGDMNTWPE 86  
QY 61 YKRRITFDITNNLSIYLALRPSDEGTGYCVLKYEKDAFKREHLAEVTLVKADFPPTS 120  
DB 87 YKRRITFDITNNLSIYLALRPSDEGTGYCVLKYEKDAFKREHLAEVTLVKADFPPTS 146  
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSMLENGEELNAINTVTSQDEPTELYAVSSKIDF 180  
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSMLENGEELNAINTVTSQDEPTELYAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHPPDN 242

RESULT 4  
US-08-751-767A-6

Sequence 6, Application US/08751767A  
Patent No. 5994104  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, ROBERT J.  
APPLICANT: GRANT, HUGH  
APPLICANT: MACDONALD, IAN D.  
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,767A  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 117-221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164091  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-751-767A-6

Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5.2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHFCSGVHYHTKEVEVATLSCGHNVSEELAQTRITYQKKEKKWLTMMSGDMNTWPE 60  
DB 27 GSHFCSGVHYHTKEVEVATLSCGHNVSEELAQTRITYQKKEKKWLTMMSGDMNTWPE 86  
QY 61 YKRRITFDITNNLSIYLALRPSDEGTGYCVLKYEKDAFKREHLAEVTLVKADFPPTS 120  
DB 87 YKRRITFDITNNLSIYLALRPSDEGTGYCVLKYEKDAFKREHLAEVTLVKADFPPTS 146  
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSMLENGEELNAINTVTSQDEPTELYAVSSKIDF 180  
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSMLENGEELNAINTVTSQDEPTELYAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHPPDN 242

RESULT 5  
US-08-153-262-2

Sequence 2, Application US/08153262  
Patent No. 6071716  
GENERAL INFORMATION:  
APPLICANT: FREEMAN, GORDON J.  
APPLICANT: NADLER, LEE M.  
APPLICANT: FREEDMAN, ARNOLD S.  
TITLE OF INVENTION: DNA Encoding B7, A New Member  
TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Dana-Farber Cancer Institute  
STREET: 44 Binney Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02115  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage  
COMPUTER: IBM Personal System 2; Model 30  
OPERATING SYSTEM: MS/DOS  
SOFTWARE: WordPerfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,262  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/751,306  
FILING DATE: 28-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HART, JULIA D.  
REGISTRATION NUMBER: 33132  
REFERENCE/DOCKET NUMBER: DFCI-116.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 255-8900  
TELEFAX: (203) 259-2846  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
FEATURE: for CD28 T cell surface antigen; transmembrane protein  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-08-153-262-2  
Query Match 100.0%; Score 1149; DB 3; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5.2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLSHFGSGVHVTKEVEKAVATLSCGHNVSELAOTRIYQKREKMYLTMSGDMNTWPE 60  
DB 27 GLSHFGSGVHVTKEVEKAVATLSCGHNVSELAOTRIYQKREKMYLTMSGDMNTWPE 86  
QY 61 YKNRTIDITNNLSIVIALRPSDGGTYECVYLKYEKDAFRREHLAEVTLVSKADFPPTS 120  
DB 87 YKNRTIDITNNLSIVIALRPSDGGTYECVYLKYEKDAFRREHLAEVTLVSKADFPPTS 146  
QY 121 ISDEPIPSNIRITCSNCGFPPEHLSWLENGEELNAINTTVSODPETELAYVSSKIDF 180  
DB 147 ISDEPIPSNIRITCSNCGFPPEHLSWLENGEELNAINTTVSODPETELAYVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHLEKVNQTFMNTTKQEHFPDN 216  
DB 207 NMTNHSFMCILIKYGHLEKVNQTFMNTTKQEHFPDN 242  
RESULT 6  
US-08-479-744A-29  
Sequence 29, Application US/08479744A  
Patent No. 6084067  
GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
TITLE OF INVENTION: No. 6084067/e1 CTLA4/CD28 Ligands and  
TITLE OF INVENTION: Uses Therefor  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,744A  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/280,757  
FILING DATE: 26-JUL-1994  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 28-AUG-1993  
APPLICATION NUMBER: 08/101,624  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 34 to 41  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
US-08-479-744A-29

Query Match 100.0%; Score 1149; DB 3; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5,2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSCGYIHTKKEKVAATISCGHNVSEELAQRIYQKKKAVLTMSGDMAIWE 60  
DB 27 GSHSCGYIHTKKEKVAATISCGHNVSEELAQRIYQKKKAVLTMSGDMAIWE 86  
QY 61 YKNTIFDTNNLSIYIALRPSDEGTGCVYKTKDAFKRHLAEVLTSAADPTPS 120  
DB 87 YKNTIFDTNNLSIYIALRPSDEGTGCVYKTKDAFKRHLAEVLTSAADPTPS 146  
QY 121 ISDFEIPISNIRIICISGSGEPPEHLSWLENGEELNAINTVSODPEELVAVSSKLD 180  
DB 147 ISDFEIPISNIRIICISGSGEPPEHLSWLENGEELNAINTVSODPEELVAVSSKLD 206  
QY 181 NMTNHSFMCILIKYGLHRYNOTFNMTTKOEHPDN 216  
DB 207 NMTNHSFMCILIKYGLHRYNOTFNMTTKOEHPDN 242

RESULT 7  
US-08-280-757B-29  
Sequence 29, Application US/08280757B  
Patent No. 6130316  
GENERAL INFORMATION:  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
APPLICANT: Gray, Gary S.  
APPLICANT: Greenfield, Edward  
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/280,757B  
FILING DATE: 26-JUL-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/101,624  
FILING DATE: 26-JULY-1993  
APPLICATION NUMBER: 08/109,393  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandagouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
US-08-280-757B-29  
Query Match 100.0%; Score 1149; DB 4; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5.2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLSHFGSVIHVTEKVEKVAATLSCGHNVSELAOTRIYWKKEKMYLTMSGDMNIMPE 60  
DB 27 GLSHFGSVIHVTEKVEKVAATLSCGHNVSELAOTRIYWKKEKMYLTMSGDMNIMPE 86  
QY 61 YKNRTIPDITNNLSIVIALRPSDEGTGYCYVLKYEKDAFKREHLAEVTLGVKADFPPTS 120  
DB 87 YKNRTIPDITNNLSIVIALRPSDEGTGYCYVLKYEKDAFKREHLAEVTLGVKADFPPTS 146  
QY 121 ISDEPIPTSNIRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELIYAVSSKIDF 180  
DB 147 ISDEPIPTSNIRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELIYAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHLPVNOTFMNNTTKOEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHLPVNOTFMNNTTKOEHPPDN 242  
RESULT 8  
US-09-159-135-2  
Sequence 2, Application US/09159135  
Patent No. 6149905  
GENERAL INFORMATION:  
APPLICANT: Ostrand-Rosenberg, Suzanne  
APPLICANT: Baskar, Sivasubramanian  
APPLICANT: Glimcher, Laurie H.  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/159,135  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/147,772  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-003  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-09-159-135-2  
Query Match 100.0%; Score 1149; DB 4; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5.2e-113; Indels 0; Gaps 0;  
Matches 216; Conservative 0; Mismatches 0;  
QY 1 GSHFCSGVIVHTKEYKEVATLSCGHNVSEELAQTRIVQKKEKKNVLTMMSGDMNIWPE 60  
DB 27 GSHFCSGVIVHTKEYKEVATLSCGHNVSEELAQTRIVQKKEKKNVLTMMSGDMNIWPE 86  
QY 61 YKRRIFDITNNLSYIYIALRPSDEGTVCYLYTKDAFKRHLAEVTLVYADPTPS 120  
DB 87 YKRRIFDITNNLSYIYIALRPSDEGTVCYLYTKDAFKRHLAEVTLVYADPTPS 146  
QY 121 ISDFEIPTSNIRITCSGSGFPEPHLSWLENGEELNATINTVSDPEPELVAVSSKIDF 180  
DB 147 ISDFEIPTSNIRITCSGSGFPEPHLSWLENGEELNATINTVSDPEPELVAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHFDDN 216  
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKQEHFDDN 242  
RESULT 9  
US-08-205-697A-19  
Sequence 19, Application US/08205697A  
Patent No. 6218510  
GENERAL INFORMATION:

```
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 629460e1 Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-19

Query Match      100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No.5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEATLSCGHNVSVEELAQTRITWQKEKKVLTMMSGDMNTIME 60
DB 27 GLSHFCGVIHVTKEVEATLSCGHNVSVEELAQTRITWQKEKKVLTMMSGDMNTIME 86
QY 61 YKRRITFDITNNLSIYLALRPSDEGTVECVLYKYEKDAKREHLAEVTLVKADFPPTS 120
DB 87 YKRRITFDITNNLSIYLALRPSDEGTVECVLYKYEKDAKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNRRITCGSGFPEPHLSWLENGEELNAINTVSODEPETELIYAVSSKLD 180
DB 147 ISDFEIPTSNRRITCGSGFPEPHLSWLENGEELNAINTVSODEPETELIYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKEHFPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKEHFPDN 242

RESULT 10
US-08-702-525-19
Sequence 19, Application US/08702525
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 629460e1 Forms of T Cell Costimulatory
TITLE OF INVENTION: Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
```

```
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-525-19

Query Match      100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No.5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVEATLSCGHNVSVEELAQTRITWQKEKKVLTMMSGDMNTIME 60
DB 27 GLSHFCGVIHVTKEVEATLSCGHNVSVEELAQTRITWQKEKKVLTMMSGDMNTIME 86
QY 61 YKRRITFDITNNLSIYLALRPSDEGTVECVLYKYEKDAKREHLAEVTLVKADFPPTS 120
DB 87 YKRRITFDITNNLSIYLALRPSDEGTVECVLYKYEKDAKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNRRITCGSGFPEPHLSWLENGEELNAINTVSODEPETELIYAVSSKLD 180
DB 147 ISDFEIPTSNRRITCGSGFPEPHLSWLENGEELNAINTVSODEPETELIYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKEHFPDN 216
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTKEHFPDN 242

RESULT 11
US-09-450-798-2
Sequence 2, Application US/09450798
Patent No. 6319709
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/450,798  
FILING DATE: 29-NOV-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,772  
FILING DATE: 03-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEDMAN, GORDON J.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-09-450-798-2  
Query Match 100.0%; Score 1149; DB 4; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5,2e-113; Mismatches 0; Indels 0; Gaps 0;  
Matches 216; Conservative 0;  
OY 1 GLSHSCGYIHTKEYKEVATILSCGHNVSVEELAQRIYQKKKAVLTMSGDMMTPE 60  
|||||  
DB 27 GLSHSCGYIHTKEYKEVATILSCGHNVSVEELAQRIYQKKKAVLTMSGDMMTPE 86  
61 YKNRTPTDITNLSYIILALRPSDEGTVCVYLKYEKDAFKREHLAEVTSVADPTPS 120  
|||||  
DB 87 YKNRTPTDITNLSYIILALRPSDEGTVCVYLKYEKDAFKREHLAEVTSVADPTPS 146  
121 ISDFEIPTSNIRRIICSTSGGPEPHLSMLNCEELNAINITVSODPETELVAVSSKIDF 180  
|||||  
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSMLNCEELNAINITVSODPETELVAVSSKIDF 206  
OY 181 NMTNHSFMCILIKYGHILRVNQTFFNMNTTQOEHPDN 216  
|||||  
DB 207 NMTNHSFMCILIKYGHILRVNQTFFNMNTTQOEHPDN 242  
RESULT 12  
US-08-403-253A-2  
Sequence 2, Application US/08403253A  
Patent No. 6352694  
GENERAL INFORMATION:  
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cell  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts



COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,253A  
FILING DATE: March 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/253,964  
FILING DATE: 3 JUNE 1994  
APPLICATION NUMBER: US 08/073,223  
FILING DATE: 4 JUNE 1993  
APPLICATION NUMBER: US 08/200,947  
FILING DATE: 23 FEB 1994  
APPLICATION NUMBER: US 07/864,805  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/247,505  
FILING DATE: 23 MAY 1994  
APPLICATION NUMBER: US 07/864,866  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 08/218,155  
FILING DATE: 25 MAR 1994  
APPLICATION NUMBER: US 07/864,807  
FILING DATE: 7 APR 1992  
APPLICATION NUMBER: US 07/902,467  
FILING DATE: 16 JUNE 1992  
APPLICATION NUMBER: US 07/275,433  
FILING DATE: 23 NOV 1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: -34 to -1  
IDENTIFICATION METHOD: amino terminal sequencing of  
IDENTIFICATION METHOD: soluble protein  
OTHER INFORMATION: hydrophobic  
FEATURE:  
NAME/KEY: extracellular domain  
LOCATION: 1 to 208  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: transmembrane domain  
LOCATION: 209 to 235  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: intracellular domain  
LOCATION: 236 to 254  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 19 to 21  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence

FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 55 to 57  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 64 to 66  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 152 to 154  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 173 to 175  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 177 to 179  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 192 to 194  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: N-linked glycosylation  
LOCATION: 198 to 200  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig V-set domain  
LOCATION: 1 to 104  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
FEATURE:  
NAME/KEY: Ig C-set domain  
LOCATION: 105 to 202  
IDENTIFICATION METHOD: similarity with known  
IDENTIFICATION METHOD: sequence  
PUBLICATION INFORMATION:  
AUTHORS: FREEDMAN, GORDON J.  
AUTHORS: FREEDMAN, ARNOLD S.  
AUTHORS: SEGIL, JEFFREY M.  
AUTHORS: LEE, GRACE  
AUTHORS: WHITMAN, JAMES F.  
AUTHORS: NADLER, LEE M.  
TITLE: B7, A New Member Of The Ig Superfamily With  
TITLE: Unique Expression On Activated And Neoplastic B Cells  
JOURNAL: The Journal of Immunology  
VOLUME: 143  
ISSUE: 8  
PAGES: 2714-2722  
DATE: 15-OCT-1989  
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
US-08-403-253A-2  
Query Match 100.0%; Score 1149; DB 4; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5,2e-113; Indels 0; Gaps 0;  
Matches 216; Conservative 0; Mismatches 0;  
Db 61 YKRRITFDITNNLSIYLALRPSDEGTVECVLKYKDAKREHLAEVTLVADPPTPS 120  
27 GLSHFGSGVHTKVEKVAATLSGHNVSVEELAQRTYQKREKAVLTMMSGDMNTWPE 86  
87 YKRRITFDITNNLSIYLALRPSDEGTVECVLKYKDAKREHLAEVTLVADPPTPS 146

QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 180  
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 242

## RESULT 13

PCT-US95-02576-19  
Sequence 19, Application PC/TUS9502576  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules  
TITLE OF INVENTION: and Uses Therefor  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02576  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/205,697  
FILING DATE: 02-Mar-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandagouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: BWI-120CPPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-02576-19

Query Match 100.0%; Score 1149; DB 5; Length 288;  
Best Local Similarity 100.0%; Pred. No. 5,2e-113;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHFCSGVHYHTKEKEVATLSCGHNVSEELAQRTIYQKCKKAVLTMMSGDMNTWPE 60  
DB 27 GSHFCSGVHYHTKEKEVATLSCGHNVSEELAQRTIYQKCKKAVLTMMSGDMNTWPE 86  
QY 61 YKRTIFDITNNLSIYIALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADPEPTPS 120  
DB 87 YKRTIFDITNNLSIYIALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADPEPTPS 146  
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 180  
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 242

## RESULT 14

US-09-171-945-131  
Sequence 131, Application US/09171945  
Patent No. 6277599  
GENERAL INFORMATION:  
APPLICANT: Emery, Stephen  
APPLICANT: Copley, Clive Graham  
APPLICANT: Edge, Michael Derek  
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
TITLE OF INVENTION: Antibody, and their Therapeutic Use in an Adept System  
FILE REFERENCE: Monoclonal Antibody to CEA  
CURRENT APPLICATION NUMBER: US/09/171,945  
CURRENT FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: GB9703103.3  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: GB9609405.7  
PRIOR FILING DATE: 1996-05-04  
PRIOR APPLICATION NUMBER: PCT/GB97/01165  
PRIOR FILING DATE: 1997-04-29  
NUMBER OF SEQ ID NOS: 131  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 131  
LENGTH: 473  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: humanized  
US-09-171-945-131

Query Match 100.0%; Score 1149; DB 4; Length 473;  
Best Local Similarity 100.0%; Pred. No. 1.1e-112;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHFCSGVHYHTKEKEVATLSCGHNVSEELAQRTIYQKCKKAVLTMMSGDMNTWPE 60  
DB 27 GSHFCSGVHYHTKEKEVATLSCGHNVSEELAQRTIYQKCKKAVLTMMSGDMNTWPE 86  
QY 61 YKRTIFDITNNLSIYIALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADPEPTPS 120  
DB 87 YKRTIFDITNNLSIYIALRPSDEGTVECVLKYEKDAFKREHLAEVTLVSKADPEPTPS 146  
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 180  
DB 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGBELNAINITVSQDEPETELAVSSKIDF 206  
QY 181 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 216  
DB 207 NMTNHSFMCILIKYGHRLVNOTFNMTTKOEHPPDN 242

## RESULT 15

US-09-460-384-36  
Sequence 36, Application US/09460384  
Patent No. 6337316  
GENERAL INFORMATION:  
APPLICANT: EL TAYAR, Nabli  
APPLICANT: BLECHNER, Steven  
APPLICANT: JAMESON, Brad  
APPLICANT: TEPPER, Mark

TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,  
PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING  
SAME  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NETMARK, P.L.L.C.  
STREET: 624 Ninth Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



